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92661

From: Huff, Sheela  
Sent: Monday, April 28, 2003 4:44 PM  
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Subject: search request for 09/682667

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Thanks-

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CRIE

Point of Contact  
P. Sheppard  
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Searcher: \_\_\_\_\_  
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Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 213 AA; 23456 MW; F8755C45CB05D626 CRC64;

Query Match 100.0%; Score 1094; DB 11; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-88;  
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MEVLRRSSVFAEIMDAFDRSPTDKELVAQAKALGREYHARLRGLSWSAPERASPAP 60
DB 1 MEVLRRSSVFAEIMDAFDRSPTDKELVAQAKALGREYHARLRGLSWSAPERASPAP 60
QY 61 GGRLAEEVCTVLLRLDDELEQIRPSYRNVAROLHIPLOSEPVTDAFLAVAGHIFSAGIT 120
DB 61 GGRLAEEVCTVLLRLDDELEQIRPSYRNVAROLHIPLOSEPVTDAFLAVAGHIFSAGIT 120
QY 121 WKKVSVLSVAAAGLAVDCVROQAPAMVHALVDCLEFVYKTTATWLRRGGWTDLKCYV 180
DB 121 WKKVSVLSVAAAGLAVDCVROQAPAMVHALVDCLEFVYKTTATWLRRGGWTDLKCYV 180
QY 181 STDGFRSHMLVATLCSFGRFKAFFLLPPER 213
DB 181 STDGFRSHMLVATLCSFGRFKAFFLLPPER 213

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## RESULT 2

Q9UL32 PRELIMINARY; PRT; 213 AA.

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AC Q9UL32:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Bcl-2 related ovarian killer.
GN BOK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hsu S.Y., Hsueh A.J.W.;
RT "CDNA cloning of the human BOK gene";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF089746; AAC09129.1; -.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
SQ SEQUENCE 213 AA; 23540 MW; 59509F8C7330517F CRC64;

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Query Match 98.4%; Score 1076; DB 4; Length 213;  
 Best Local Similarity 98.6%; Pred. No. 7.2e-87;  
 Matches 210; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MEVLRRSSVFAEIMDAFDRSPTDKELVAQAKALGREYHARLRGLSWSAPERASPAP 60
DB 1 MEVLRRSSVFAEIMDAFDRSPTDKELVAQAKALGREYHARLRGLSWSAPERASPAP 60
QY 61 GGRLAEEVCTVLLRLDDELEQIRPSYRNVAROLHIPLOSEPVTDAFLAVAGHIFSAGIT 120
DB 61 GGRLAEEVCTVLLRLDDELEQIRPSYRNVAROLHIPLOSEPVTDAFLAVAGHIFSAGIT 120
QY 121 WKKVSVLSVAAAGLAVDCVROQAPAMVHALVDCLEFVYKTTATWLRRGGWTDLKCYV 180
DB 121 WKKVSVLSVAAAGLAVDCVROQAPAMVHALVDCLEFVYKTTATWLRRGGWTDLKCYV 180
QY 181 STDGFRSHMLVATLCSFGRFKAFFLLPPER 213
DB 181 STDGFRSHMLVATLCSFGRFKAFFLLPPER 213

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RESULT 3  
 Q9UMX3 PRELIMINARY; PRT; 212 AA.

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AC Q9UMX3:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE BCL-2-related ovarian killer protein (Similar to BCL-2-related ovarian
DE killer protein-like-PENDING) (BCL-2-related ovarian killer
DE protein-like).
GN BOK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang H.;
RT "Gene expression of a human homolog of BCL-2-related ovarian killer
RT protein.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174487; AAD51719.1; -.
DR EMBL; BC006203; AAH06203.1; -.
DR EMBL; BC017214; AAH17214.1; -.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
SQ SEQUENCE 212 AA; 23280 MW; 053ED605FE8F5B2 CRC64;

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Query Match 94.7%; Score 1035.5; DB 4; Length 212;  
 Best Local Similarity 95.3%; Pred. No. 2.6e-83;  
 Matches 203; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

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QY 1 MEVLRRSSVFAEIMDAFDRSPTDKELVAQAKALGREYHARLRGLSWSAPERASPAP 60
DB 1 MEVLRRSSVFAEIMDAFDRSPTDKELVAQAKALGREYHARLRGLSWSAPERASPAP 60
QY 61 GGRLAEEVCTVLLRLDDELEQIRPSYRNVAROLHIPLOSEPVTDAFLAVAGHIFSAGIT 120
DB 61 GGRLAEEVCTVLLRLDDELEQIRPSYRNVAROLHIPLOSEPVTDAFLAVAGHIFSAGIT 119
QY 121 WKKVSVLSVAAAGLAVDCVROQAPAMVHALVDCLEFVYKTTATWLRRGGWTDLKCYV 180
DB 121 WKKVSVLSVAAAGLAVDCVROQAPAMVHALVDCLEFVYKTTATWLRRGGWTDLKCYV 179
QY 181 STDGFRSHMLVATLCSFGRFKAFFLLPPER 213
DB 181 STDGFRSHMLVATLCSFGRFKAFFLLPPER 212

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## RESULT 4

Q91812 PRELIMINARY; PRT; 213 AA.

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AC Q91812:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Bcl-2-related ovarian killer protein.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

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OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20487164; PubMed=11034351.  
 RA Zhang H., Holzgreve W., De Geyter C.;  
 RT "Evolutionarily conserved Bcl proteins in the Bcl-2 family."  
 RL FEBS Lett. 480:311-313(2000).  
 DR EMBL; AF275944; AAF81282.1; .  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; BCL-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; P550062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 213 AA; 23619 MW; B3AF7049P25442E3 CRC64;

Query Match 81.5%; Score 892; DB 13; Length 213;  
 Best Local Similarity 78.4%; Pred. No. 1,le-70;  
 Matches 167; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

OY 1 MEVLRSSVFAAEIMDAFDRSPTDKELVAQAALGREYVHARLLRAGLSWSAPERASAP 60  
 DB 1 MEVLRSSVFAAEVMEVFRSPTDKELVQAALCRDYINSRLIRAGVSMSPKPHNTVPV 60  
 OY 61 GGRLAEVCVTLRLGDELQIRPSYRNAROLHIPILOSEPVYTDALFLAVAGHIFSAGIT 120  
 DB 61 GGRLAEVSAILLRLGDELEYIRPNRYRNAROLNLSHSETVYTDALFLAVAAQIFTAGIT 120  
 OY 121 WGVVSVLSVAAGLAVDCVROAPAMVHALVDCLEFVKRTLATWLRRGWTDVLCYV 180  
 DB 121 WGVVSVLSVAAGLAVDCVROAPAMVHITVDCLEFVKRTLATWLRRGWTDVLCYV 180  
 OY 181 STDPCGRSHMLVATLCSFGFRLKAAFFLLPPER 213  
 DB 181 STDPCGRSHMLVAAVCSFGFRLKAAFFLLPPER 213

RESULT 5  
 OY9DCJ5 PRELIMINARY; PRT; 213 AA.

ID O9DCJ5;  
 AC O9DCJ5;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Bcl-2-related ovarian killer protein.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Mills E.M., Johnson A.L., Bridgman J.T.;  
 RT "Characterization and Expression of Bcl in the Hen Ovary."  
 RL Submitted (Jun-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF290888; AAG01182.1; .  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR002475; BCL2\_FAMILY.  
 DR Pfam: PF00452; BCL-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; P550062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 213 AA; 23658 MW; 07CC06BEBD7311EC CRC64;

Query Match 81.0%; Score 886; DB 13; Length 213;  
 Best Local Similarity 77.5%; Pred. No. 3,6e-70;  
 Matches 165; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

OY 1 MEVLRSSVFAAEIMDAFDRSPTDKELVAQAALGREYVHARLLRAGLSWSAPERASAP 60  
 DB 1 MEVLRSSVFAAEVMEVFRSPTDKELVQAALCRDYINSRLIRAGVSMSPKPHNTVPV 60  
 OY 61 GGRLAEVCVTLRLGDELQIRPSYRNAROLHIPILOSEPVYTDALFLAVAGHIFSAGIT 120  
 DB 61 GGRLAEVSAILLRLGDELEYIRPNRYRNAROLNLSHSETVYTDALFLAVAAQIFTAGIT 120

DB 61 GGRLAEVSAILLRLGDELEYIRPNRYRNAROLNLSHSETVYTDALFLAVAAQIFTAGIT 120  
 OY 121 WGVVSVLSVAAGLAVDCVROAPAMVHALVDCLEFVKRTLATWLRRGWTDVLCYV 180  
 DB 121 WGVVSVLSVAAGLAVDCVROAPAMVHITVDCLEFVKRTLATWLRRGWTDVLCYV 180  
 OY 181 STDPCGRSHMLVATLCSFGFRLKAAFFLLPPER 213  
 DB 181 STDPCGRSHMLVAAVCSFGFRLKAAFFLLPPER 213

RESULT 6  
 ID 088857 PRELIMINARY; PRT; 170 AA.  
 AC 088857;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Bcl-2-related ovarian killer protein.  
 GN BCL.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=OVARY;  
 RA MEDLINE=98024143; PubMed=9356461;  
 RA Hsu S.Y., Kaipia A., McGee E., Lomeli M., Hsueh A.J.W.;  
 RT "Bcl-2 is a pro-apoptotic bcl-2 protein with restricted expression in reproductive tissues and heterodimerizes with selective anti-apoptotic bcl-2 family members."  
 RT Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).  
 RN [2]  
 RP TISSUE=OVARY;  
 RC SEQUENCE FROM N.A.

RA Hsu S.Y., Hsueh A.J.W.;  
 RT "A splicing variant of the Bcl-2 member Bcl-2 with a truncated BH3 domain induces apoptosis without dimerization with anti-apoptotic Bcl-2 proteins."  
 RT Submitted (Feb-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF051093; AAC61928.1; .  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR002475; BCL2\_FAMILY.  
 DR Pfam: PF00452; BCL-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; P550062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 170 AA; 18729 MW; 15E54361F448CF16 CRC64;

Query Match 77.4%; Score 846.5; DB 11; Length 170;  
 Best Local Similarity 79.8%; Pred. No. 8,2e-67;  
 Matches 170; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

OY 1 MEVLRSSVFAAEIMDAFDRSPTDKELVAQAALGREYVHARLLRAGLSWSAPERASAP 60  
 DB 1 MEVLRSSVFAAEIMDAFDRSPTDKELVAQAALGREYVHARLLRAGLSWSAPERASAP 60  
 OY 61 GGRLAEVCVTLRLGDELQIRPSYRNAROLHIPILOSEPVYTDALFLAVAGHIFSAGIT 120  
 DB 61 GGRLAEVCVTLRLGDELQIRPSYRNAROLHIPILOSEPVYTDALFLAVAGHIFSAGIT 120  
 OY 121 WGVVSVLSVAAGLAVDCVROAPAMVHALVDCLEFVKRTLATWLRRGWTDVLCYV 180  
 DB 121 WGVVSVLSVAAGLAVDCVROAPAMVHALVDCLEFVKRTLATWLRRGWTDVLCYV 180  
 OY 181 STDPCGRSHMLVATLCSFGFRLKAAFFLLPPER 213  
 DB 181 STDPCGRSHMLVATLCSFGFRLKAAFFLLPPER 213

RESULT 7  
 ID 09V9C8 PRELIMINARY; PRT; 300 AA.

AC Q9V9C8; 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DE 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DEATH EXECUTIONER Bcl-2 homolog protein (PROAPOPTOTIC Bcl-2 homolog  
DEBCL) (Bcl-2 family member protein) (Bcl-2 ORTHOLOG DBORG-1).  
GN DBORG-1 OR BOK OR BCL2 OR Bcl OR ROB-1 OR CG12397.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=EMBRYO;  
RX MEDLINE=20105529; PubMed=2015529;  
RA Igaki T., Kanuka H., Inohara N., Sawamoto K., Nunez G., Okano H.,  
RA Miura M.;  
RT "Drob-1, a Drosophila member of the Bcl-2/CED-9 family that promotes  
RT cell death.";  
RT Proc. Natl. Acad. Sci. U.S.A. 97:662-667(2000).  
RN [2]  
RP REVISIONS TO N-TERMINUS.  
RA Igaki T., Kanuka H., Inohara N., Sawamoto K., Okano H., Miura M.;  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20155510; PubMed=10684252;  
RA Coussei P.A., Quinn L.M., Huang D.C.S., Coombe M., Read S.H.,  
RA Richardson H., Kumar S.;  
RT "Debcl, a proapoptotic Bcl-2 homologue, is a component of the  
RT Drosophila melanogaster cell death machinery.";  
RT J. Cell Biol. 148:703-714(2000).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Zhang H., Huang Q., Ke N., Matsuyama S., Hammock B., Godzik A.,  
RA Reed J.C.;  
RT "Drosophila pro-apoptotic Bcl-2/Bax homolog reveals evolutionary  
RT conservation of cell death mechanisms.";  
RT J. Biol. Chem. 276:40000-40006(2001).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Schier S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt J., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Botkin K.C., Botchan M.R., Boulton J., Brokstein P., Brotlier P.,  
RA Butts K.C., Busam D.A., Butler H., Cardew E., Center A., Chandra I.,  
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fodor C., Gabriellian A.E., Gang N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idagyan C.,  
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kelchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
RA Palenzuela M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Palzetta K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,  
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.-N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RT Science 287:2185-2195(2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RA Kurada P., White K.;  
RT "Putative Drosophila homolog of mammalian Bcl-2-related ovarian killer  
RT protein.";  
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RA Zhou L., Steller H.;  
RT "Potential Drosophila homologue of Bcl-2-related ovarian killer  
RT (BOK).";  
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP SEQUENCE FROM N.A.  
RA Brachmann C.B., Jassim O.W., Wachsmuth B.D., Cagan R.L.;  
RT "Dorg-1, a Drosophila Bcl-2 family member that functions in the  
RT apoptotic response to UV-irradiation.";  
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP EMBL; AB032430; BAA89603.2; -  
RT EMBL; AF149798; AAF26841.1; ALT\_INIT.  
RN [10]  
RP EMBL; AF178430; AAF62819.1; -  
RT EMBL; AF228044; AAF89185.1; -  
RN [11]  
RP EMBL; AF228044; AAF89185.1; -  
RT EMBL; AF228044; AAF89185.1; -  
RN [12]  
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RT EMBL; AF228044; AAF89185.1; -  
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RT EMBL; AF228044; AAF89185.1; -  
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RN [26]  
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RT EMBL; AF228044; AAF89185.1; -  
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RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003825; AAF58628.1; -  
 DR HSSP: 007817; 1MA2.  
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 DR InterPro: IPR000712; BCL2\_BH.  
 DR Pfam: PF00452; BCL2\_family.  
 DR SMART: SM00337; BCL2.  
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 DB 87 QDIISGRLCGHYTKRRRLRSGLTKLGLORISLSTSMGIVRDVFPAYQVYGLDEL 146  
 OY 79 EOIRSVYRNVAROL-----HIPLQSEPVYTDALVAGHIFSAGITGKVSLSY 130  
 DB 147 EHMHRITNGVARQICRNPGSEFHP---DAVSLLAGVAGELRVELTWSKVISLRF 202  
 OY 131 AAGLAVDCVRAQAPMAHALVDCICEFVRKTLATMLRRRGW 172  
 DB 203 AGGLSVDCVROGHPYLPKLMESEVEIDELVPMINENGW 244

## RESULT 11

ID 095083 PRELIMINARY; PRT; 317 AA.  
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 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE GH01265P  
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 OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
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 RA Champe M., Chavez C., Dorsett V., Farfan D., Flise E., George R.,  
 RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY058249; AAL13478.1; -  
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 DR InterPro: IPR000712; BCL2\_BH.  
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 DB 96 DINDGKCLCGYIRARLRKRGVLRKYTORLRNTLDPSGHVVEVPALMSGEELER 155  
 OY 81 IRPSYRNVAROL-HIP---LQSEPVYTDALVAGHIFSAGITGKVSLSYAGLAV 136  
 DB 156 MHRVYTNISQLSRAPGELSDMAMMLNLVAKDLFRSSITWGKIISIFAVCGFAI 215

OY 137 DCVROAPAMVHALVDCICEFVRK--TLATWLRRRG 171  
 DB 216 DCVROGHEFDYQLDIDGLAEITGRGLADRRGRWVG 252

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ID 035843 PRELIMINARY; PRT; 235 AA.  
 AC 035843;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE BCL2-gamma.  
 GN BCL2L.  
 OS *Mus musculus* (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B6/CBA; TISSUE=THYMUS;  
 RX MEDLINE=98051053; PubMed=9390687;  
 RA Yang X.-F., Weber G.F., Cantor H.;  
 RT "A novel Bcl-2 isoform connected to the T cell receptor regulates  
 RT apoptosis in T cells";  
 RL Immunity 7:629-639(1997).  
 DR EMBL: U51277; AAC53458.1; -  
 DR HSSP: P53563; 1AR3.  
 DR MGD: MGI:88139; Bcl2l.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH.  
 DR InterPro: IPR002475; BCL2\_FAMILY.  
 DR InterPro: IPR004725; BCL2\_reg.  
 DR Pfam: PF00452; BCL2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL2; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRfam: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1; 1.  
 DR PROSITE: PS0063; BH4\_2; 1.  
 SO SEQUENCE 235 AA; 26122 MW; 649D914C2D5378F6 CRC64;

Query Match 14.5%; Score 159; DB 11; Length 235;  
 Best Local Similarity 22.3%; Pred. No. 3.3e-06;  
 Matches 52; Conservative 31; Mismatches 80; Indels 70; Gaps 8;

OY 21 SPTDELVQAQALREYVHARLLRAGLSMS-----APERA----- 56  
 DB 2 SQSNRELAV-----DPLSYLQSGYWSQFSDVEENRTEAPETEAERTPSAINGN 54  
 OY 57 -----SPAPGR-----LAEVCYLLRLGDELQIRSVYRNVAROLHI 95  
 DB 55 PSHMLADSPAVNGATGHSSSLDAREYIPMAAYKALREAGDFELRYRAESDLTSQHT 114  
 OY 96 PLQSEPVYTDALVAGHIFSAGITGKVSLSYAGLAVDCVRAQAPMAHALVDCIG 155  
 DB 115 ---TGTAIVQSTFEQVYNELFRGVMGRIVAFFSGALCVSVKQGVLSRLASMA 171  
 OY 156 EFRKTLATWLRRRGW-----TDVLCVYSTDPGFRSH-----WLVAT 194  
 DB 172 TYLNLHLEPFIQENGWGVSGTPLRSYFRRLVQY-PCVAEHVCDPSLMEVET 223

## RESULT 13

ID 092386 PRELIMINARY; PRT; 236 AA.  
 AC 092386;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

```

DE B-cell lymphoma protein 2.
GN BCL2.
OS Cricetulus longicaudatus (long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxId=10030;
RN [1]
RP SEQUENCE FROM N.A.
RA Lai D.Z., Chen W., Wang H.T.;
RT "Construction of a robust CHO cell line for biopharmaceutical use.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBD databases.
DR EMBL; AF404339; AAK92201.1; -.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; Bcl2_family.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR TIGRFAMs: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; UNKNOWN_1.
DR PROSITE: PS01258; BH2; UNKNOWN_1.
DR PROSITE: PS01259; BH3; UNKNOWN_1.
DR PROSITE: PS01260; BH4_1; UNKNOWN_1.
DR PROSITE: PS50063; BH4_2; 1.
SQ SEQUENCE 236 AA; 26500 MW; BEDF052EF32CA8B8 CRC64;

Query Match 14.2%; Score 155; DB 11; Length 236;
Best Local Similarity 21.8%; Pred. No. 7.5e-06;
Matches 47; Conservative 35; Mismatches 78; Indels 56; Gaps 7;

OY 28 VQAQKALG-----REYVHARLLRAGLSW-----SAPERASPAFG-----QIHT-P 96
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MAQAGRTGYDNREIVMKYHYKLSQGYEMDGDVDAALGAPPTGIFSGFPESNPTPA 60

OY 62 -----GRLAEVCTVLLRLGDELEQIRPSYRNVAR-----QIHT-P 96
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 VHRDMAKRSPLRPVATGPTLSPVPVYHLLRLRRAGDFSRHYRDEAFEMSSQLHLP 120

OY 97 LOSEPVTDAFLVAGHIFSAGITGKVVSLYSVAAGLAVDCVROAQPAMVHALVDCIG 156
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 FTRK----GRTAVVEELPRDGVNMGRIYAFFFGVCMCVESYNREKSPLVDAIALMTE 176

OY 157 FVAKTLATWLRRRGWTDLKCV-VSTDPGRSHWL 191
   : : : | | | : | | : : | | | |
DB 177 YLNRHLHTWLIQDNGMDAFVELYGPVRLPDEFSWL 212

RESULT 14
O9QWXM2 PRELIMINARY; PRT; 188 AA.
AC O9QWXM2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Bcl-x (Fragment).
GN BCL2L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20350651; PubMed-10894153;
RX Wyszewski B. III, Dietzsch P., Wagner K.U., Garrett L.,
RT "Bcl-x and Bax regulate mouse primordial germ cell survival and
apoptosis during embryogenesis.";
RL Mol. Endocrinol. 14:1038-1052(2000).
DR EMBL; AF088904; AAC72232.1; -.
DR HSSP; P53563; IAF3.
DR MGD; MGI:88139; Bcl2L.

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DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS50063; BH4_2; 1.
FT NON_TER 188
SQ SEQUENCE 188 AA; 21126 MW; 4E62F8356D248E52 CRC64;

Query Match 14.1%; Score 154.5; DB 11; Length 188;
Best Local Similarity 22.3%; Pred. No. 6.3e-06;
Matches 44; Conservative 29; Mismatches 69; Indels 55; Gaps 5;

OY 21 SPDKELVQAQKALGREYVHARLLRAGLSWS-----APERA----- 56
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2 SQSNRELIV-----DFLSYKLSQGYSMQSFSDVENTETAPDETAEARETPSALNGN 54

OY 57 -----SPAQGR-----LAEVCTVLLRLGDELEQIRPSYRNVARQIHT 95
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 55 PSWHLADSPAVNGATGSHSSLDAREVIYPMAAVQALREAGDEFEELRYRRAFSDLSQLHT 114

OY 96 PLQSEPVYDAFLVAGHIFSAGITGKVVSLYSVAAGLAVDCVROAQPAMVHALVDCIG 155
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 115 ---TPGTAVQSFQVAVNELRDGVNMGRIYAFPSFGALCVESVDKEMOVLASRIASWMA 171

OY 156 EFVRKTLATWLRRRGCM 172
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 172 TYINDHLEPWIQENGCM 188

RESULT 15
O35844 PRELIMINARY; PRT; 233 AA.
AC O35844;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Bcl-xL.
GN BCL2L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-B6/CBA; TISSUE=THYMUS;
RX MEDLINE-98051053; PubMed-9390687;
RA Yang X.-F., Weber G.F., Cantor H.;
RT "A novel Bcl-x isoform connected to the T cell receptor regulates
apoptosis in T cells.";
RL Immunity 7:629-639(1997).
DR EMBL; U51278; AAC53459.1; -.
DR HSSP; P53563; IAF3.
DR MGD; MGI:88139; Bcl2L.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.

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DR PROSITE; PS01260; BH4_1; 1.  
DR PROSITE; PS50063; BH4_2; 1.  
SQ SEQUENCE 233 AA; 26033 MW; 3083F2D8327E072E CRC64;
```

Query Match	14.1%;	Score 154.5;	DB 11;	Length 233;
Best Local Similarity	22.3%;	Pred. No. 8.2e-06;		
Matches 44;	Conservative 29;	Mismatches 69;	Indels 55;	Gaps 5;

```

Oy 21 SPTDELYAQAOKALGREGVHARRLLRAGISMS-----APER-----56
      |:::|
Db 2 SOSNRELIV-----DPLSKLSOKGYSMSQSDVEENRTAEPEETAEERPPSALINGN 54
Oy 57 -----SPABGR-----LAEVCTVLLRIGDELOIRPPSYRRVARLOHI 95
      |||
Db 55 PSMHLADSPAVNGATGHSSSLDAREVIYPMVAVKALAEADDEFELRRARFSDLTSLHI 114
      |||
Oy 96 PLOSPPVYTDLFLVAGHIISAGITWGVVSLSYAAGLAVDCYRQAOAPMHVHALDCLG 155
      |:::|
Db 115 --PPTAYOSFEQVYVNEFLFRDGNMGRIYAFESFGALCVESYDKEMOVLVSRIASMA 171
Oy 156 EFVRKTLATWLRBRGGW 172
      ::|
Db 172 TYLNDHEPWIQENGW 188

```

Search completed: April 29, 2003, 11:25:39.  
Job time : 29.2507 secs

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2003, 11:18:26 ; Search time 7.50783 Seconds

(without alignments)  
1176.699 Million cell updates/sec

Title: US-09-682-667-2

Perfect score: 1094

Sequence: 1 MEVLRRSSVFIAEIMDAFDR.....TLCSPGRFIKAFLLPER 213

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164.5	15.0	236	1 BCL2_RAT	P49950 ratu
2	161.5	14.8	229	1 BCL2_BOVIN	002718 bos
3	156.5	14.3	236	1 BCL2_CRITO	093178 cric
4	154.5	14.1	233	1 BCLX_MOUSE	064373 mus
5	154.5	14.1	233	1 BCLX_MOUSE	P53563 ratu
6	154.5	14.1	236	1 BCL2_MOUSE	P10417 mus
7	152.5	13.9	228	1 ARL_XENLA	091827 xen
8	152.5	13.9	233	1 BCL2_CHICK	000709 gall
9	150.5	13.8	233	1 BCLX_HUMAN	007817 homo
10	150.5	13.8	233	1 BCLX_PIG	077737 sus
11	150.5	13.8	239	1 BCL2_HUMAN	P10415 homo
12	149.5	13.7	218	1 BAXB_HUMAN	007814 homo
13	144.5	13.2	192	1 BAXA_HUMAN	007812 homo
14	141.5	12.9	229	1 BCLX_CHICK	007816 gall
15	139.5	12.8	204	1 ARL1_XENLA	091828 xen
16	136	12.4	208	1 BAX_MOUSE	008734 mus
17	135.5	12.4	193	1 BCLM_MOUSE	P70345 mus
18	134.5	12.3	192	1 BAXA_BOVIN	002703 bos
19	132	12.1	211	1 BAK_HUMAN	016611 homo
20	131.5	12.0	193	1 BCLM_HUMAN	092843 homo
21	130.5	11.9	192	1 BAXA_MOUSE	003690 ratu
22	130.5	11.9	192	1 BAXA_MOUSE	003690 ratu
23	127	11.6	211	1 BAK2_HUMAN	013014 homo
24	117	10.7	350	1 MCL1_HUMAN	007820 homo
25	111.5	10.2	143	1 BAXD_HUMAN	P55269 homo
26	93.5	8.5	172	1 BFL1_MOUSE	007440 mus
27	93.5	8.5	115	1 BCLM_MOUSE	007440 mus
28	92.5	8.5	175	1 BCLM_MOUSE	007440 mus
29	84.5	7.7	672	1 ACBA_PHYBL	015648 homo
30	84.5	7.7	1121	1 CARB_MYCLE	09cc22 myco
31	84	7.7	177	1 NR13_COTJA	090343 cotu
32	83	7.6	941	1 DNAB_RHOMR	030477 rhod
33	82	7.5	551	1 SMA4_MOUSE	P97471 mus

34	82	7.5	552	1 SMA4_HUMAN	013485 homo
35	82	7.5	552	1 SMA4_PIG	090439 sus
36	82	7.5	552	1 SMA4_PIG	070437 ratu
37	81.5	7.4	311	1 PCAO_AGR5	P52668 agri
38	81	7.4	1081	1 CARB_SYNY3	055756 syn
39	80.5	7.4	2003	1 NTC4_HUMAN	094466 homo
40	79.5	7.3	406	1 WCAL_SALTY	P26388 salm
41	79	7.2	205	1 GTSL_ASCSU	P46436 asca
42	79	7.2	312	1 MTA_SPRCO	069967 stre
43	78	7.1	501	1 CP2B_RAT	035132 ratu
44	77.5	7.1	319	1 MOCB_STNP7	056208 syn
45	77.5	7.1	385	1 RURE_PSEOL	P17052 pseud

## ALIGNMENTS

RESULT 1	ID	Sequence	STANDARD	PRT	236 AA
BCL2_RAT	AC	P49950: 062837; 064032;			
BCL2_RAT	DT	01-OCT-1996 (Rel. 34, Created)			
BCL2_RAT	DT	01-NOV-1997 (Rel. 35, Last sequence update)			
BCL2_RAT	DT	15-JUN-2002 (Rel. 41, Last annotation update)			
BCL2_RAT	DE	Apoptosis regulator Bcl-2.			
BCL2_RAT	GN	BCL2 OR BCL-2.			
BCL2_RAT	OS	Rattus norvegicus (Rat).			
BCL2_RAT	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
BCL2_RAT	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
BCL2_RAT	OX	NCBI_TaxID=10116;			
BCL2_RAT	RN	[1]			
BCL2_RAT	RP	SEQUENCE FROM N.A.			
BCL2_RAT	RC	TISSUE=Brain;			
BCL2_RAT	RX	MEDLINE=94193015; PubMed=8144041;			
BCL2_RAT	RA	Sato T., Irie S., Krajewski S., Reed J.C.;			
BCL2_RAT	RT	"Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";			
BCL2_RAT	RL	Gene 140:291-292(1994).			
BCL2_RAT	RL	[2]			
BCL2_RAT	RP	SEQUENCE FROM N.A.			
BCL2_RAT	RC	STRAIN=Sprague-Dawley; TISSUE=Ovary;			
BCL2_RAT	RX	MEDLINE=95129487; PubMed=7828536;			
BCL2_RAT	RA	Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;			
BCL2_RAT	RT	"Expression of members of the bcl-2 gene family in the immature rat			
BCL2_RAT	RT	ovary: equine chorionic gonadotropin-mediated inhibition of granulosa			
BCL2_RAT	RT	cell apoptosis is associated with decreased bax and constitutive			
BCL2_RAT	RT	bcl-2 and bcl-xlong messenger ribonucleic acid levels.";			
BCL2_RAT	RL	Endocrinology 136:232-241(1995).			
BCL2_RAT	RN	[3]			
BCL2_RAT	RP	SEQUENCE OF 19-172 FROM N.A.			
BCL2_RAT	RX	MEDLINE=95059917; PubMed=7969891;			
BCL2_RAT	RA	Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,			
BCL2_RAT	RT	Lindholm D.;			
BCL2_RAT	RT	"bcl-2 messenger RNA is localized in neurons of the developing and			
BCL2_RAT	RT	adult rat brain.";			
BCL2_RAT	RL	Neuroscience 61:165-177(1994).			
BCL2_RAT	CC	-1- FUNCTION: Suppresses apoptosis in a variety of cell systems			
BCL2_RAT	CC	including factor-dependent lymphohematopoietic and neural cells.			
BCL2_RAT	CC	Regulates cell death by controlling the mitochondrial membrane			
BCL2_RAT	CC	permeability. Appears to function in a feedback loop system with			
BCL2_RAT	CC	caspases. Inhibits caspase activity either by preventing the			
BCL2_RAT	CC	release of cytochrome c from the mitochondria and/or by binding to			
BCL2_RAT	CC	the apoptosis-activating factor (APAF-1).			
BCL2_RAT	CC	-1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and			
BCL2_RAT	CC	Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2			
BCL2_RAT	CC	domains, and is necessary for anti-apoptotic activity (By			
BCL2_RAT	CC	similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).			
BCL2_RAT	CC	-1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular			
BCL2_RAT	CC	membrane of the nuclear envelope and the endoplasmic reticulum.			
BCL2_RAT	CC	-1- TISSUE SPECIFICITY: Expressed in a variety of tissues, with			
BCL2_RAT	CC	highest levels in reproductive tissues. In the adult brain,			
BCL2_RAT	CC	expression is localized in mitral cells of the olfactory bulb,			
BCL2_RAT	CC	granule and pyramidal neurons of hippocampus, pontine nuclei,			
BCL2_RAT	CC	cerebellar granule neurons, and in ependymal cells. In prenatal			





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CC -----
DR EMBL: U92434; AAB53319.1; -
DR HSSP: 007817; 1MA2.
DR InterPro: IPR002475; Bcl2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfams: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS50063; BH4_2; 1.
DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
KW DOMAIN 10 30 BH4.
FT DOMAIN 64 68 POLY-PRO.
FT DOMAIN 69 72 POLY-ALA.
FT DOMAIN 83 97 BH3.
FT DOMAIN 126 145 BH1.
FT DOMAIN 177 192 BH2.
FT TRANSMEM 202 223 POTENTIAL.
FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT MOD_RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ SEQUENCE 229 AA; 25099 MW; ADIDDAF96FFFIID CRC64;

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Query Match 14.8%; Score 161.5; DB 1; Length 229;
Best Local Similarity 23.1%; Pred. No. 1.4e-07;
Matches 49; Conservative 35; Mismatches 77; Indels 51; Gaps 7;

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QY 37 EYVHARILRAGLSW-----SAPERASAPG-----GLAE----- 66
DB 17 KIIHKLISRGYEMDAGADGAAAPGAPAPGILSSQPGRTAPASRTSPPPPAAGAPAP 76
QY 67 -----VCTVLRIGDELBOIRPSYRVNAROLHI-PLQSEPVVTPDAFLVAGHIPSAGI 119
DB 77 SEVPPVVTILTRQAGDDFERRRTRRDPFAEMSSQHLTFPTAR-----ERFATVVEELFRDGV 132
QY 120 TWGKVVSLXSVAGLAVDVRQAQPMVAHVLDCEFEVRKTLATWLRRRGMTDVLKCV 179
DB 133 NMGRIYAFEEFGVMKVEFVSNREMSPLVDISIALMTEYINRHLHTWIONGMDARVELY 192
QY 180 -VSTDGFRSHLVATLCSFGRPLKAAFULL 210
DB 193 GPMRPLDFEWSL-----SLKALLSLAL 215

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## RESULT 3

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BCL2_CRILLO STANDARD; PRT; 236 AA.
AC Q9JTV8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Citicellus longicaudatus (long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Citicellus.
OX NCBI_TaxId=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RX MEDLINE=20431763; PubMed=10973819;
RA Tomicic M.T., Christman M., Kaina B.;
RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2
  protein.";
RL Biochem. Biophys. Res. Commun. 275:899-903(2000).

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RN [2]
RP SEQUENCE FROM N.A. AND CLEAVAGE BY CASPASES.
RX MEDLINE=21092839; PubMed=11181062;
RA Tomicic M.T., Kaina B.;
RT "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9
  and caspase-3.";
RL Biochem. Biophys. Res. Commun. 281:404-408(2001).
CC -I- FUNCTION: Suppresses apoptosis in a variety of cell systems
  including factor-dependent lymphohematopoietic and neural cells.
  Regulates cell death by controlling the mitochondrial membrane
  permeability. Appears to function in a feedback loop system with
  caspases. Inhibits caspase activity either by preventing the
  release of cytochrome c from the mitochondria and/or by binding to
  the apoptosis-activating factor (Apaf-1) (By similarity).
CC -I- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAK and
  Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
  domains, and is necessary for anti-apoptotic activity (By
  similarity). Also interacts with Apaf-1 and RA-1 (By similarity).
CC -I- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
  membrane of the nuclear envelope and the endoplasmic reticulum.
CC -I- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
  for interaction with RA-1 (By similarity).
CC -I- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
  anti-apoptotic activity. Growth factor-stimulated phosphorylation
  on Ser-70 by PKC is required for the anti-apoptosis activity and
  occurs during the G2/M phase of the cell cycle (By similarity). In
  the absence of growth factors, Bcl2 appears to be phosphorylated
  by other protein kinases such as ERKs and stress-activated kinases
  (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A)
  (By similarity).
CC -I- PTM: Proteolytically cleaved by caspases during apoptosis. The
  cleaved protein, lacking the BH4 domain, has pro-apoptotic
  activity, causes the release of cytochrome c into the cytosol
  promoting further caspase activity.
CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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  the European Bioinformatics Institute. There are no restrictions on its
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AJ271720; CAB92245.1; -
DR HSSP: 007817; 1MA2.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfams: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS50063; BH4_2; 1.
KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
FT DOMAIN 10 30 BH4.
FT DOMAIN 64 68 POLY-PRO.
FT DOMAIN 69 72 POLY-ALA.
FT DOMAIN 83 97 BH3.
FT DOMAIN 126 145 BH1.
FT TRANSMEM 202 223 POTENTIAL.
FT SITE 34 35 CLEAVAGE (BY CASPASE-3 AND CASPASE-9).
FT MOD_RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

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SO SEQUENCE 236 AA; 26491 MW; BECADPIEE3337228 CXC64;
Query Match 14.3%; Score 156.5; DB 1; Length 236;
Best Local Similarity 22.4%; Pred. No. 4.2e-07;
Matches 50; Conservative 36; Mismatches 80; Indels 57; Gaps 8;

OY 28 VAOAALG-----REYVHARLNLAGLSW-----SAPERSAPAG----- 61
DB 1 MAQAGRTGYDNRRELYMKIYHYLSRGTEEMVDYGDVADAPLGAAPTPGIFSFOPESNPPTPA 60
OY 62 -----GRLAEYCTVLLRLGDELEQIRPSVYRNVAR-----OLHI-P 96
DB 61 VHRDMAATSPRLRPVATVTGPTLSPVPVPHLLTLRRADDGFSRRYRDRPFAEMXSQHLILP 120
OY 97 LQSEPVVDAFLAVNGHTEFSGITGKGVVSLYSVAAGLAVDCVRAQAMAHVALVDCE 156
DB 121 FTAR----GRRATVVEELFRDGVNMGRIYAFEEFGVGVCEVSNEMSPDLNIALMTE 176
OY 157 FVRKTLATWLRRRGGWTDVLKCV-VSTDGERSHWL-VATLCS 197
DB 177 YLNRLHTWIDNGMGWDAFVELYGPSPRLPFDGFSWLSTKLTL 219

RESULT 4
BCLX_MOUSE STANDARD; PRT; 233 AA.
ID BCLX_MOUSE STANDARD; PRT; 233 AA.
AC Q64373; Q60657; Q60658; Q61338;
DC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-x.
GN BCL2L1 OR BCL2L2 OR BCLX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=244B;
RC Kameski H., Michaud G.Y., Takatsu K., Okuma M.;
RC submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN RL [2]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
RC STRAIN=CS7BL/6; TISSUE=Brain;
RC MEDLINE=95311139; PubMed=7607090;
RX Gonzalez-Garcia M., Perez-Ballesteros R., Ding L., Duan L., Boise L.H.,
RX Thompson C.B., Nunez G.;
RT "bcl-xL is the major bcl-x mRNA form expressed during murine
RT development and its product localizes to mitochondria."
RT J. Immunol. 120:3033-3042(1994).
RN RL [3]
RP SEQUENCE FROM N.A. (ISOFORMS X(L); X(S) AND X(Delta-TM)).
RC TISSUE=Pre-B cell;
RC MEDLINE=95052604; PubMed=7963517;
RX Fang W., Rivard J.J., Mueller D.L., Behrens T.W.;
RT "Cloning and molecular characterization of mouse bcl-x in B and T
RT lymphocytes."
RT J. Immunol. 153:4388-4398(1994).
RN RL [4]
RP SEQUENCE FROM N.A. (ISOFORM X(BETA)).
RC STRAIN=CS7BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=98051053; PubMed=9390687;
RX Yang X.-F., Weber G.F., Cantor H.;
RT "A novel Bcl-x isoform connected to the T cell receptor regulates
RT apoptosis in T cells."
RT Immunol. 7:629-639(1997).
RN RL [5]
RP SEQUENCE FROM N.A.
RC MEDLINE=97289584; PubMed=9144489;
RX Grillot D.A., Gonzalez-Garcia M., Ehteraee D., Duan L., Inohara N.,
RX Ohta S., Seidman M.F., Nunez G.;
RT "Genomic organization, promoter region analysis, and chromosome
RT localization of the mouse bcl-x gene."

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FT TRANSMEM 210 226 POTENTIAL.
FT VARSPLIC 126 188 MISSING (IN ISOFORM BCL-X(S)).
FT VARSPLIC 189 233 DTEVDLYGNNAAESRKGQERNRFLTGTVAGVLLGSL
FT VARSPLIC 194 233 FSRK -> VRTTLPVCPPLACVSLCEHP (IN ISOFORM
FT VARSPLIC 194 233 BCL-X(BETA)).
FT VARSPLIC 194 233 LYGNNAAESRKGQERNRFLTGTVAGVLLGSLFSRK
FT VARSPLIC 194 233 -> GHDCGMCAGSLTLQSEVVRH (IN ISOFORM BCL-
FT VARSPLIC 194 233 X(DELTA-TM)).
SQ SEQUENCE 233 AA; 26132 MW; 242DAC79887E072E CRC64;

Query Match 14.1%; Score 154.5; DB 1; Length 233;
Best Local Similarity 22.3%; Pred. No. 6.3e-07;
Matches 44; Conservative 29; Mismatches 69; Indels 55; Gaps 5;

QY 21 SPTDELVAQAKAGREYVHARLLRAGLSMS-----APEPA----- 56
DB 2 SOSNRELVV-----DELSTKLSOKGYSMQSFQSDVEENRTAPETEARETPSAINGN 54
QY 57 -----SPAPGCR-----LAECVTLLRLGDELEQIRPSVYRNVARQLHI 95
DB 55 PSWMHLADSPAVNGATGCHSSSLDAREVTPMAVKQALREAGDEFLRYRAFDLSQLHI 114
QY 96 PLOSEPVTDAFLAVAGHIFSGAGITGWKVVSLYSVAAGLAIVDCVQAOAPAMVHALVDCIG 155
DB 115 --TFGTAYQSEFEQVYVNEFLFDGVNMGRIVAFSEFGALCVESVDKEMQVLVSRIASMA 171
QY 156 EFVVRTLATWLRRRGGW 172
DB 172 TYLNDHLEPWIQENGW 188

RESULT 5
BCLX_RAT STANDARD: PRT: 233 AA
AC P53563; Q62678; P70614; P70613; Q62836; Q64087; Q64128;
BT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-x.
GN BCL2L1 OR BCL2L OR BCLX.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN 11
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC TISSUE-Brain;
RA Michaelidis T.M.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RA Wesselingh S.L., David G.L., Choi S., Veltona M., Hardwick J.M.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
RC TISSUE-Thymus;
RA Shiraeva N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Ohta S.;
RL "An additional form of rat Bcl-x, Bcl-xbeta, generated by an
RT unspliced RNA, promotes apoptosis in promyeloid cells.";
RN J. Biol. Chem. 271:13258-13265(1996).
RN 14
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC STRAIN-Sprague-Dawley; TISSUE-Ovary;
RA MEDLINE=95129487; PubMed=7828536;
RN Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT "Expression of members of the bcl-2 gene family in the immature rat
RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT cell apoptosis is associated with decreased bax and constitutive
RT bcl-2 and bcl-x long messenger ribonucleic acid levels.";
RN Endocrinology 136:232-241(1995).
RN 15

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RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=98010630; PubMed=9346936;
RA Arlotto M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,
RA Morikawa K.;
RT "Crystal structure of rat Bcl-XL. Implications for the function of
RT the Bcl-2 protein family.";
RL J. Biol. Chem. 272:27886-27892(1997).
CC -1 FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC caspases (By similarity). Appears to regulate cell death by
CC blocking the voltage-dependent anion channel (VDAC) by binding
CC to it and preventing the release of the caspase activator,
CC cytochrome c, from the mitochondrial membrane. The Bcl-x(S) and
CC Bcl-x(beta) isoforms promote apoptosis.
CC -1 SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC similarity). Heterodimerization with BAX does not seem to be
CC required for anti-apoptotic activity (By similarity).
CC -1 SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC ENVELOPE (BY SIMILARITY).
CC -1 ALTERNATIVE PRODUCTS: 3 ISOFORMS: BCL-X(L) (SHOWN HERE), BCL-X(S)
CC AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1 TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS
CC SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE
CC OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT
CC DETECTABLE LEVEL OF BCL-X(S).
CC -1 DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization
CC with other Bcl2 family members and for repression of cell death.
CC -1 PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity (By similarity).
CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1 SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X82537; CAAS7886.1; -
DR EMBL; X82537; CAAS7887.1; -
DR EMBL; U10579; AAI19257.1; -
DR EMBL; U72350; AAB17353.1; -
DR EMBL; U72349; AAB17352.1; -
DR EMBL; U34963; AAA77686.1; -
DR EMBL; S76513; AAC60701.1; ALT_INIT.
DR EMBL; S78284; AAC60702.1; -
DR PDB; 1AF3; 07-JUL-97.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR003093; BCL2_BH4.
DR InterPro: IPR004725; BCL2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMS; TIGR00865; bcl-2; 1.
DR PROSITE; PS01062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS00063; BH4_2; 1.
KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
3D-structure.
FT DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.

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FT DOMAIN 180 195 BH2
FT TRANSMEM 210 226 POTENTIAL.
FT VARSPPLIC 126 188 MISSING (IN ISOFORM BCL-X(S)).
FT VARSPPLIC 189 233 DTFVLDGNNAAESRGOEFNMFPLTGMVAGVILGSL
FT 189 233 FSRK -> VRTPLRCPLVLSVSELPNCFMSPGVVED
FT 189 233 IDYSGDIPGL (IN ISOFORM BCL-X(BETA)).
FT CONFLICT 6 6 R -> Q (IN REF. 1).
FT CONFLICT 12 12 F -> S (IN REF. 2).
FT CONFLICT 64 64 A -> E (IN REF. 2).
FT CONFLICT 81 81 I -> L (IN REF. 4).
FT CONFLICT 119 119 A -> V (IN REF. 4).
FT CONFLICT 143 144 FF -> SS (IN REF. 4).
FT CONFLICT 199 199 A -> T (IN REF. 4).
FT CONFLICT 201 201 A -> P (IN REF. 4).
SQ SEQUENCE 233 AA; 26158 MW; 2B62BC63864BC9F CRC64;

Query Match 14.1%; Score 154.5; DB 1; Length 233;
Best Local Similarity 22.3%; Pred. No. 6.3e-07;
Matches 44; Conservative 29; Mismatches 69; Indels 55; Gaps 5;

QY 21 SPTRKELVAQKALGREYVHARLLRAGLSWS-----APERA----- 56
2 SOSNRRLV-----DELSTYKLSQKGSMSQSFDEENRTPEDETEPERETPSAINGN 54
QY 57 -----SPARGR-----LAECVYLLRLGDELQIRSVYRNARQLHI 95
55 PSMHLADSPVANGATGSSSIDAREVTPMAAVKQALREAGDEFFELRYRRASDLTSLHI 114
QY 96 PLOSEPVYTDALFVAGHIFSGAGITWGKVSLSVAAGLADVCVROAOPAWHALVDLIG 155
115 ---TPGTAQSGFEQGVNLFKFDGVNMGRIVAFSGGALCVESVDKENGQVLSRASMA 171
QY 156 EFVRKTLATWLRNRGGW 172
172 TYLNDHLEPWIOENGW 188

Db 172 TYLNDHLEPWIOENGW 188

RESULT 6
BCL2_MOUSE STANDARD; PRT; 236 AA.
ID BCL2_MOUSE P10417; P10418;
AC P10417; P10418;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2 OR BCL-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC STRAIN-BALB/C; TISSUE=Liver;
RA MEDLINE=87187643; PubMed=3032455;
RA Negri M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.;
RT "Molecular analysis of bcl-2: structure and expression of the murine
RT gene homologous to the human gene involved in follicular lymphoma.";
RL Cell 49:455-463(1987).
RN [2]
RP REVISIONS TO 221-222.
RX MEDLINE=92375724; PubMed=1508712;
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression
RT in a variety of tissues including lymphoid and neuronal organs in
RT adult and embryo.";
RL Nucleic Acids Res. 20:4187-4192(1992).
RN [3]
RP PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.
RX MEDLINE=97277291; PubMed=9115213;
RA Ito T., Deng X., Carr B., May W.S. Jr.;
RT "Bcl-2 phosphorylation required for anti-apoptosis function.";
RL J. Biol. Chem. 272:11671-11673(1997).
RN [4]

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RP DEPHOSPHORYLATION BY PP2A.
RX MEDLINE=99069407; PubMed=9852076;
RA Deng X., Ito T., Carr B., Mumbly M., May W.S. Jr.;
RT "Reversible phosphorylation of Bcl2 following interleukin 3 or
RT bryostatine 1 is mediated by direct interaction with protein
RT phosphatase 2A*.";
RL J. Biol. Chem. 273:34157-34163(1998).
CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (Apaf-1).
CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity (By
CC similarity). Also interacts with APAF-1 and RAIF-1.
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;
CC are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAIF-1.
CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle. In the absence of
CC growth factors, Bcl2 appears to be phosphorylated by other protein
CC kinases such as ERKs and stress-activated kinases.
CC Dephosphorylated by protein phosphatase 2A (PP2A).
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L31532; AAA37282.1; -
DR EMBL; M16506; AAA37282.1; JOINED.
DR EMBL; M16506; AAA37281.1; -
DR PIR; A25960; TVMSAL.
DR PIR; B25960; TVMSAL.
DR PIR; E37332; E37332.
DR HSP; Q07817; IMAZ.
DR HSP; MGI:88138; BCL2.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR004725; Bcl2_Reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFSMS; TIGR00865; bcl-2; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS01260; BH4_2; 1.
DR PROSITE; PSS0063; BH4_2; 1.

```

KM Apoptosis; Alternative splicing; Transmembrane; Mitochondrion;  
 KM Phosphorylation.  
 FT DOMAIN 10 30 BH4.  
 FT DOMAIN 90 104 BH3.  
 FT DOMAIN 133 152 BH1.  
 FT DOMAIN 184 199 BH2.  
 FT TRANSMEM 209 230 POTENTIAL.  
 FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
 FT MOD.RES 70 70 PHOSPHORYLATION (BY PKC).  
 FT VARSPIC 193 236 DAFVELGFSMRPLEDFSLSKITLSTLALVACITLGLAYL  
 GKK -> VQACIVE (IN ISOFORM BETA).  
 SQ SEQUENCE 236 AA; 26425 MW; AAB5EFB076BE0A CRC64;  
 Query Match 14.1%; Score 154.5; DB 1; Length 236;  
 Best local similarity 22.4%; Pred. No. 6.4e-07;  
 Matches 50; Conservative 36; Mismatches 80; Indels 57; Gaps 8;  
 QY 28 VQAQALG-----REYVHARLLRAGLSW-----SAPERASPAAG----- 61  
 DB 1 MAQAGRTGYDNREIVAKKIHVKLSRGYEMDAGDADAAPLGAAPATGIFSFQESNMPRA 60  
 QY 62 -----GRLAEVCTVLLRLGDELEQIRPSYRNVAR-----QHT-P 96  
 DB 61 VHEMARARSPRLPVAATGAPALSPVPCVHLTLRRAGDQFSRRYRDRFAEMSSQLHLRP 120  
 QY 97 LQSEPVVTAFLAVAGHIFSAGITWCKVSLYSVAAGLAVDCVQAQAPAMVHALVDCLE 156  
 DB 121 FAR-----GRLATVVEELTRDQVCMGRIVAFPEFGVMCEVSNREMSPLVDIALMTE 176  
 QY 157 EVRKTLATWLRRRGWTDLKCV-VSTDGFSNHWL-VATLCS 197  
 DB 177 YINRHLHTWIDONGWDFAVELYGPMSRPLDFSMILSKTLIS 219  
 RESULT 7  
 ARL\_XENLA  
 ID ARL\_XENLA STANDARD: PRT; 228 AA.  
 AC 091827;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator R1 (XRL) (fragment).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8335;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Head;  
 RX MEDLINE=95331613; PubMed=7607538;  
 RA Cruz-Reyes J., Tata J.R.;  
 RT "Cloning, characterization and expression of two Xenopus bcl-2-like  
 cell-survival genes.";  
 RL Gene 138:171-179(1995).  
 CC -1- FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W.  
 CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).  
 CC -1- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE  
 CC BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND  
 CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC EMBL: X82462; CAA57845.1; .

DR HSP: C007817; 1MA2.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH4.  
 DR Pfam: PF0452; BCL-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR Apoptosis; Transmembrane.  
 FT NON\_TER 1 1  
 FT DOMAIN 120 139 BH1.  
 FT DOMAIN 171 186 BH2.  
 FT TRANSMEM 207 227 POTENTIAL.  
 SQ SEQUENCE 228 AA; 25068 MW; C499DA49A585F8A9 CRC64;  
 Query Match 13.9%; Score 152.5; DB 1; Length 228;  
 Best local similarity 23.7%; Pred. No. 9.3e-07;  
 Matches 40; Conservative 30; Mismatches 74; Indels 25; Gaps 5;  
 QY 20 RSPDKELVAQ-----AKALGREYVHARLLRAGLSWSAPERASPAAGRLAEVC-- 68  
 DB 28 RGSPPDKYLTREQGMAQSDGLSRALVEDLVRYKLCQPSL-----VPEPSG--AASCAL 77  
 QY 69 -TYLRLGDELEQIRPSYRNVARQLHPLQSEPVVTAFLAVAGHIFSAGITWCKVSL 127  
 DB 78 HSMARAGDEFEERFQASSEISTQIHV--PGTAVARFAEYAGSLFQGVNMGRIYAF 134  
 QY 128 YSAAGLAVDCVQAQAPAMVHALVDCLEGFVRKTLATWLRRRGWTDL 176  
 DB 135 FVEGALCAESVKNKEMSPLLPRIQDMVWYLETENLMDWQSGNGMGFL 183  
 RESULT 8  
 BCL2\_CHICK  
 ID BCL2\_CHICK STANDARD: PRT; 233 AA.  
 AC 000709;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2 OR BCL-2.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92375724; PubMed=1508712;  
 RA Eguchi Y., Ewert D.L., Tsujimoto Y.;  
 RT "Isolation and characterization of the chicken bcl-2 gene: expression  
 RT in a variety of tissues including lymphoid and neuronal organs in  
 RT adult and embryo.";  
 RL Nucleic Acids Res. 20:4187-4192(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=B-cell lymphoma;  
 RX MEDLINE=92379084; PubMed=1511008;  
 RA Cazals-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;  
 RT "Molecular cloning and DNA sequence analysis of cDNA encoding chicken  
 RT homologue of the Bcl-2 oncoprotein.";  
 RL Biochim. Biophys. Acta 1132:109-113(1992).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (Apaf-1).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and



CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (By similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane. The Bcl-x(s)  
 CC isoform promotes apoptosis.  
 CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2.  
 CC Heterodimerization with BAX does not seem to be required for anti-  
 CC apoptotic activity.  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
 CC ENVELOPE (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S)  
 CC AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS  
 CC THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING  
 CC LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING  
 CC LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.  
 CC -1- DOMAIN: The B4 domain is required for anti-apoptotic activity.  
 CC The B1 and B2 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the B4 domain, has pro-apoptotic  
 CC activity.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: 223116; CAAB0662.1; -  
 CC EMBL: 223115; CAAB0661.1; -  
 CC EMBL: U72398; AAB17354.1; -  
 CC PDB: 1BXL; 29-OCT-97.  
 CC PDB: 1LXL; 21-APR-97.  
 CC PDB: 1MAZ; 21-APR-97.  
 CC Genew: HGNC:992; BCL2L1.  
 CC MIM: 600039; -  
 CC InterPro: IPR002475; BCL2\_family.  
 CC InterPro: IPR000712; Bcl2\_BH.  
 CC InterPro: IPR003093; Bcl2\_BH4.  
 CC InterPro: IPR004725; Bcl2\_reg.  
 CC Pfam: PF00452; Bcl-2; 1.  
 CC Pfam: PF02180; BH4; 1.  
 CC SMART: SM00337; BCL; 1.  
 CC SMART: SM00265; BH4; 1.  
 CC TIGRfam: TIGR00865; bcl-2; 1.  
 CC PROSITE: PS0062; BCL2\_FAMILY; 1.  
 CC PROSITE: PS01080; BH1; 1.  
 CC PROSITE: PS01258; BH2; 1.  
 CC PROSITE: PS01259; BH3; 1.  
 CC PROSITE: PS01260; BH4\_1; 1.  
 CC PROSITE: PS0063; BH4\_2; 1.  
 CC Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;  
 CC 3D-structure.  
 CC FT DOMAIN 4 24 BH4.  
 CC FT DOMAIN 86 100 BH3.  
 CC FT DOMAIN 129 148 BH1.  
 CC FT DOMAIN 180 195 BH2.  
 CC FT TRANSMEM 210 226 POTENTIAL.  
 CC FT SITE 61 61 CLEAVAGE BY CASPASE-1.  
 CC FT VARSPPLIC 126 188 MISSING (IN ISOFORM BCL-X(S)).  
 CC FT VARSPPLIC 189 233 DFEVELYGNNAAESRKGRENRFLTCMTVAGVVLGLSL  
 CC FT VARSPPLIC 189 233 FSRK -> VRTKPLVCPFLASQSRPTALLLYLFLCWVI  
 CC FT VARSPPLIC 189 233 VGVDVS (IN ISOFORM BCL-X(BETA)).  
 CC FT MUTAGEN 61 61 D->A: NO CLEAVAGE BY CASPASE-1 NOR BY

FT MUTAGEN 131 133 CASPASE-3.  
 FT MUTAGEN 135 137 FRD->VRA: NO HETERODIMERIZATION WITH BAX.  
 FT MUTAGEN 138 140 VNM->AIL: LOSS OF ANTI-APOPTOTIC  
 FT MUTAGEN 138 140 ACTIVITY.  
 FT MUTAGEN 138 140 GRI->ELN: LOSS OF ANTI-APOPTOTIC  
 FT MUTAGEN 138 140 ACTIVITY.  
 FT MUTAGEN 138 140 G->A: NO HETERODIMERIZATION WITH BAX.  
 FT MUTAGEN 148 148 G->E: NO HETERODIMERIZATION WITH BAX.  
 FT MUTAGEN 156 156 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT MUTAGEN 176 176 WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY  
 FT MUTAGEN 188 189 BY ABOUT HALF.  
 FT MUTAGEN 189 189 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT CONFLICT 70 70 G -> A (IN REF. 1; CAAB0661).  
 SO SEQUENCE 233 AA; 26049 MM; E09D3CDD851AE3BE CRC64;  
 Query Match 13.8%; Score 150.5; DB 1; Length 233;  
 Best Local Similarity 22.3%; Pred. No. 1,4e-06;  
 Matches 44; Conservative 29; Mismatches 69; Indels 55; Gaps 5;  
 QY 21 SPDKELVAQAKLAGREYVHARLLRAGLSMS-----APER----- 56  
 DB 2 SOSNRELV-----DFLSYKLSQKGYSMQSDVEENRTEAEGTESMETPSAINGN 54  
 QY 57 -----SPAGGR-----LAECVTLRLGDELEQIRPSYRYNARQIHI 95  
 DB 55 PSMHLADSPAVNGATGCHSSSLDAREVIMPAVQALREADEFELRRARFSDITSQIHI 114  
 QY 96 PLOSEPVYTAFLAVAGHITSAGITGCKVYSLYSVAGLAVDCVQAQPMVHALDCLG 155  
 DB 115 ---TPGTAYGSFRDGVNLEFRDGVNMGRIVAFESFGALCVESDKEMQVLVSRIAMMA 171  
 QY 156 EFVFKTLATWLRRCGW 172  
 DB 172 TYLNDHLEPWIOENGW 188  
 RESULT 10  
 BCLX\_PIG STANDARD; PRT; 233 AA.  
 ID BCLX\_PIG  
 AC 077737;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-x.  
 GN BCL2L1 OR BCL2L OR BCLX.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99171363; PubMed=10072723;  
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;  
 RT "Quantification of cardioprotective gene expression in porcine  
 RT short-term hibernating myocardium";  
 RL J. Mol. Cell. Cardiol. 31:147-158(1999).  
 CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (By similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane.  
 CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By  
 CC similarity). Heterodimerization with BAX does not seem to be  
 CC required for anti-apoptotic activity (By similarity).  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
 CC ENVELOPE (By similarity).  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
 CC The BH1 and BH2 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis (By  
 CC similarity). The cleaved protein, lacking the BH4 domain, has pro-  
 CC apoptotic activity (By similarity).





including factor-dependent lymphohematopoietic and neural cells.  
 Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (Apaf-1).  
 -1 SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and BCL-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with Apaf-1 and RAf-1.  
 -1 SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.  
 -1 ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta; are produced by alternative splicing.  
 -1 TISSUE SPECIFICITY: Expressed in a variety of tissues.  
 -1 DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAf-1.  
 -1 PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.  
 -1 PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity.  
 -1 DISEASE: Involved in follicular lymphoma (FL) (also known as type II chronic lymphatic leukemia) by a chromosomal translocation t(14;18)(q32;q21) which involves Bcl2 and Immunoglobulin gene regions.  
 -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 -1 DATABASE: BELONGS TO THE BCL-2 FAMILY.  
 -1 NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;  
 WWW="http://www.infobiogen.fr/services/Chromancer/Genes/BCL2ID49.htm".  
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 -----  
 DR EMBL: M13994; AAA51813.1; ALT\_SEQ.  
 DR EMBL: M13995; AAA51814.1; ALT\_SEQ.  
 DR EMBL: M14745; AAA35591.1; -  
 DR EMBL: X06487; CAA29778.1; -  
 DR EMBL: S72602; AAD14111.1; ALT\_SEQ.  
 DR PIR: A29409; TVHUA1.  
 DR PIR: B29409; TVHOB1.  
 DR PIR: A24428; TVHOB1.  
 DR PIR: C37332; C37332.  
 DR PIR: D37332; D37332.  
 DR HSSP: C07817; IMAZ.  
 DR Genew: HGNC:990; BCL2.  
 DR MIM: 151430; -  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH4.  
 DR InterPro: IPR004725; BCL2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMS: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 KW Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane;  
 KW Mitochondrion; Phosphorylation; Chromosomal translocation;  
 KW Polymorphism; Disease mutation.  
 FT DOMAIN 10 30  
 FT DOMAIN 93 107  
 FT DOMAIN 136 155  
 FT DOMAIN 187 202  
 FT TRANSMEM 212 233  
 FT SITE 34 35  
 FT MOD\_RES 70 70  
 FT VARSPIC 196 239  
 FT VARIANT 7 7  
 FT VARIANT 59 59  
 FT VARIANT 93 93  
 FT VARIANT 93 93  
 FT MUTAGEN 34 34  
 FT MUTAGEN 64 64  
 FT MUTAGEN 145 145  
 FT MUTAGEN 188 188  
 FT CONFLICT 48 48  
 FT CONFLICT 59 59  
 FT CONFLICT 117 117  
 FT CONFLICT 129 129  
 SO SEQUENCE 239 AA; 26266 MW; 3C49F2B714DC9C64;  
 Query Match 13.8%; Score 150.5; DB 1; Length 239;  
 Best Local Similarity 21.9%; Pred. No. 1.5e-06;  
 Matches 46; Conservative 36; Mismatches 75; Indels 53; Gaps 7;  
 QY 37 EYVHARLRLAGLSM-----SAPERASPARG-----GRLAECT--- 69  
 DB 17 KYIHYRLSQRGYEMDAGVGAAPGAPGIRSSOPGHTPHPAASRDPAKTSPLQTPA 76  
 QY 70 -----VLRIGDELEOIRPSVYRNVARQLHI-PLQSEPVTDAFLA 109  
 DB 77 APCAAGPALSPVPVPHVHLTRQAGDDFSRRYRDPAEMSSQHLHPFNAR-----GRTAT 132  
 QY 110 VAGHFSAGITWCKVYSLSVANGLAVDYCRQAPMVAHVLVDCLEFVAKTTLATWLR 169  
 DB 133 VVELFRDGVNMGRIYAFFEFGGVCESVNRMSPLVDNIALMTETYLNRHLHTWIQDN 192  
 QY 170 GGTWDLVKCV-VSTDPGFSHML-VATICS 197  
 DB 193 GGDVAFVELYGPMSRPLDFPSWLSKTLTLLS 222  
 RESULT 12  
 BAXB\_HUMAN  
 ID BAXB\_HUMAN STANDARD; PRT; 218 AA.  
 AC 007814;  
 DT 01-FEB-1995 (rel. 31, Created)  
 DT 01-FEB-1995 (rel. 31, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE Apoptosis regulator BAX, cytoplasmic isoform beta.  
 GN BAX.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-B-cell;  
 RX MEDLINE=93364978; PubMed=8358790;

```

RA Oliva Z.N., Millman C.L., Korsmeyer S.J.:  

RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that  

RT accelerates programmed cell death.";  

RL Cell 74:609-619(1993).  

CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND  

CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS  

CC HOMOLOG E1B 19K PROTEIN.  

CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,  

CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND AL.  

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  

CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOTORM ALPHA AND THE THREE  

CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY  

CC ALTERNATIVE SPLICING.  

CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  

CC -1- DOMAIN: INTERACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND  

CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION  

CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.  

CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMODOLOGY 1 (BH1) DOMAIN.  

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMODOLOGY 2 (BH2) DOMAIN.  

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMODOLOGY 3 (BH3) DOMAIN.  

CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  

CC -----  

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CC or send an email to license@isb-sib.ch).  

CC -----  

DR EMBL; L22474; AAA03620.1; .  

DR PIR; B47538; B47538.  

DR HSSP; O07817; IMAZ.  

DR Genew; HGNC:959; BAX.  

DR MIM; 600040; .  

DR InterPro; IPRO02475; BCL2_family.  

DR InterPro; IPRO00712; BCL2_BH.  

DR Pfam; PF00452; Bcl-2; 1.  

DR SMART; SM00337; BCL_1.  

DR PROSITE; PS01080; BH1; 1.  

DR PROSITE; PS01258; BH2; 1.  

DR PROSITE; PS01259; BH3; 1.  

DR PROSITE; PS50062; BCL2_FAMILY; 1.  

KW Apoptosis; Alternative splicing.  

FT DOMAIN 59 73 BH3.  

FT DOMAIN 98 118 BH1.  

FT DOMAIN 150 165 BH2.  

SQ SEQUENCE 218 AA; 24220 MW; F69DCD70F960192P CRC64;  

Query Match 13.7%; Score 149.5; DB 1; Length 218;  

Best local similarity 28.8%; Pred. No. 1.6e-06;  

Matches 46; Conservative 29; Mismatches 72; Indels 13; Gaps 6;  

QY 22 PTDELYVAQAALGRE-VYHARKLLRAGLSWSAPERA-SPAP-GGRLAECVTLRLGDEL 78  

DB 13 PTSSFOIKMTGALLLOGFIDPRAGRMG--GEAPELALDPVPDASTKKLSCELRIGDEL 70  

QY 79 EOIRSRYRNVARQRIHILOSEPVYTDAFLAVAGIIFESAG-ITWGKVSYLSVAGGLAVD 137  

DB 71 DS-----NNELODMAIAVDTSDFEEFFFAADMFSDGNFMNGRVALLFYFAFKVLK 123  

QY 138 CVROAPAMVALVDCLEAFVKTKLATLVRRRGCTDVLIK 177  

DB 124 ALCTKVPKLITIMGWTLDFLRRLTGNIODGGGVRLIK 163  

RESULT 13  

ID BAXA_HUMAN STANDARD: PRT; 192 AA.  

AC 007812:  

FT 01-FEB-1995 (Rel. 31, Created)  

FT 01-FEB-1995 (Rel. 31, Last sequence update)
```

DE 15-JUN-2002 (Rel. 41, Last annotation update)  
DR Apoptosis regulator BAX, membrane isoform alpha.  
CN BAX.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;.  
RX MEDLINE=93364978; PubMed=8358790;  
RA Oliva Z.N., Millman C.L., Korsmeyer S.J.;  
RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that  
RL accelerates programmed cell death.";  
RN cell 74:609-619(1993).  
[2]  
RN MUTAGENESIS, AND FUNCTION OF BH3 DOMAIN.  
RX MEDLINE=96091131; PubMed=8521816;  
RA Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,  
RT Elangovan B., Chinnadurai G., Lutz R.J.;  
RT "A conserved domain in Bax, distinct from BH1 and BH2, mediates cell  
RL death and protein binding functions.";  
RN EMBO J. 14:5589-5596(1995).  
[3]  
RN VARIANT PLASMACYTOMA GU-11, VARIANT T-CELL ACUTE LYMPHOBLASTIC  
RP LEUKEMIA ARG-67, AND VARIANT BURKITT LYMPHOMA VAL-108.  
RX MEDLINE=96200607; PubMed=9531611;  
RA Meljertink J.P.P., Mensink E.J.B.M., Wang K., Sedlak T.W.,  
RT Sloetjes A.W., de Witte T., Waksman G., Korsmeyer S.J.;  
RT "Haematopoietic malignancies demonstrate loss-of-function mutations of  
RL BAX.";  
RN Blood 91:2991-2997(1998).  
CC -I- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND  
CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS  
CC HOMOLOG ELB 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,  
CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.  
CC -I- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,  
CC ELB 19K PROTEIN, BCL-X(L), MCL-1 AND A1.  
CC -I- SUBCELLULAR LOCATION: Membrane-bound.  
CC -I- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE  
CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY  
CC ALTERNATIVE SPLICING.  
CC -I- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  
CC -I- DOMAIN: INTERACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND  
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION  
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.  
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.  
CC -I- DISEASE: Defects in BAX are found in some cell lines from  
CC haematopoietic malignancies as T-cell acute lymphoblastic leukemia,  
CC Burkitt lymphoma, and plasmacytoma.  
CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
CC -I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC  
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CC  
DR EMBL: L22473; AAA03619.1; -  
DR PIR: A47538; A47538.  
DR HSSP: Q07817; IMAZ.  
DR Genew: HGNC:959; BAX.  
DR MIM: 600040; -  
DR InterPro: IPR002475; BCL2\_family.  
DR InterPro: IPR000712; BCL2\_BH.  
DR Pfam: PF00452; BCL-2; 1.  
DR SMART: SM00357; BCL; 1.  
DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
DR

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DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
KM Apoptosis; Anti-oncogene; Transmembrane; Alternative splicing;
Disease mutation.
FT DOMAIN 59 73 BH3.
FT DOMAIN 98 118 BH1.
FT DOMAIN 150 165 BH2.
FT TRANSMEM 172 192 POTENTIAL.
FT VARIANT 11 11 G -> E (IN PLASMACYTOMA).
FT VARIANT 67 67 /FTID-VAR_013575.
FT VARIANT 67 67 G -> R (IN T-CELL ACUTE LYMPHOBLASTIC
LEUKEMIA; LOSS OF HETERODIMERIZATION WITH
BCL-2 OR BCL-X(L)).
FT FTID-VAR_007809.
FT VARIANT 108 108 G -> V (IN BURKITT LYMPHOMA; LOSS OF
HOMODIMERIZATION).
FT FTID-VAR_013576.
SQ SEQUENCE 192 AA; 21184 MW; 6C0CDB0A7DEE4994 CRC64;

Query Match 13.2%; Score 144.5; DB 1; Length 192;
Best Local Similarity 28.3%; Pred. No. 4e-06;
Matches 45; Conservative 29; Mismatches 72; Indels 13; Gaps 6;

OY 22 PTDKELVAQAKALGRE-YVHARLLRAGLSWSPERA-SPAP-GGRLAEVCTVLLRLGDEL 78
| | : : : : : | | | | : : : : : | | | | : : : : :
| | : : : : : | | | | : : : : : | | | | : : : : :
DB 13 PTSEQIMTGTALLGFGFIQDRAGRMG--GEAPELADPVPQDASTKLSKCRIGDEL 70
| | : : : : : | | | | : : : : : | | | | : : : : :
| | : : : : : | | | | : : : : : | | | | : : : : :
OY 79 EQIRPSYRNVARQLHIPLQSEPVYTDAPLAAGHIFSG-ITWGVSLYSVAAGLAND 137
| | : : : : : | | | | : : : : : | | | | : : : : :
| | : : : : : | | | | : : : : : | | | | : : : : :
DB 71 DS-----NMELQRMIAAVDTPDSREVEFRVAADMSQENFMGVVALFYFASKLVLK 123
| | : : : : : | | | | : : : : : | | | | : : : : :
| | : : : : : | | | | : : : : : | | | | : : : : :
OY 138 CVRQAPAMVHALVDCLEFEVFKTLATWLRRCGWTDLV 176
| | : : : : : | | | | : : : : : | | | | : : : : :
| | : : : : : | | | | : : : : : | | | | : : : : :
DB 124 ALCTKYPELIRITMGWTLDFRLRLGLQIDOGGNDGL 162
| | : : : : : | | | | : : : : : | | | | : : : : :
| | : : : : : | | | | : : : : : | | | | : : : : :

RESULT 14
BCIX.CHICK STANDARD: PRT; 229 AA.
ID BCIX.CHICK
AC 007816; Q98908;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-X.
GN BCL2L1 OR BCLX OR BCL-X.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (SHORT FORM).
RX MEDLINE=93364977; PubMed=8358789;
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
of apoptotic cell death.";
RT Cell 74:597-608(1993).
RL [2]
RN [2]
RP SEQUENCE FROM N.A. (LONG FORM).
RX STRAIN=Hubbard White Mountain; TISSUE=Testis;
RX MEDLINE=97264485; PubMed=9110311;
RA Vilagrasa X., Mezquita C., Mezquita J.;
RT "Differential expression of bcl-2 and bcl-x during chicken
spermatogenesis.";
RT Mol. Reprod. Dev. 47:26-29(1997).
CC -1- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
CC ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANS AND PERINUCLEAR
CC ENVELOPE (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A

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CC CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
CC DEVELOPMENT.
CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC FUNCTION. INTRACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC APOPTOTIC ACTIVITY (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC CC
CC EMBL: Z23110; CAAB0657.1; -
CC EMBL: U26645; AAB07677.1; -
CC PIR: A47537; A47537.
CC DR HSSP: P53563; 1A83.
CC DR InterPro: IPR002475; BCL2_family.
CC DR InterPro: IPR000712; BCL2_BH.
CC DR InterPro: IPR003093; BCL2_BH4.
CC DR InterPro: IPR004725; BCL2_reg.
CC DR Pfam: PF00452; BCL-2; 1.
CC DR Pfam: PF02180; BH4; 1.
CC DR SMART: SM00337; BCL; 1.
CC DR SMART: SM00265; BH4; 1.
CC DR TIGRFS: TIGR00865; bcl-2; 1.
CC DR PROSITE: PS50062; BCL2_FAMILY; 1.
CC DR PROSITE: PS01080; BH1; 1.
CC DR PROSITE: PS01258; BH2; 1.
CC DR PROSITE: PS01259; BH3; 1.
CC DR PROSITE: PS01260; BH4; 1.
CC DR PROSITE: PS50063; BH4_2; 1.
CC KM Apoptosis; Transmembrane; Alternative splicing.
CC FT DOMAIN 4 24 BH4.
CC FT DOMAIN 82 96 BH3.
CC FT DOMAIN 125 144 BH1.
CC FT DOMAIN 176 191 BH2.
CC FT TRANSMEM 206 223 POTENTIAL.
CC FT VARSPIC 185 229 ERFVLDYGNNAELRKQGETENKMLTGATVAGVLLGSL
FT FT LSRK -> VRTLP (IN SHORT ISOFORM).
SQ SEQUENCE 229 AA; 25733 MW; A97D3A4D04C0E9DA CRC64;

Query Match 12.9%; Score 141.5; DB 1; Length 229;
Best Local Similarity 22.3%; Pred. No. 9.2e-06;
Matches 43; Conservative 30; Mismatches 69; Indels 51; Gaps 5;

OY 21 SPDKELVAQAKALGREYVHARLLRAGLSWSPERA-SPAP-GGRLAEVCTVLLRLGDEL 111
| | : : : : : | | | | : : : : : | | | | : : : : :
| | : : : : : | | | | : : : : : | | | | : : : : :
DB 2 SSSNREIYI-----DFVSKYLSQGHCHSELEEDENTDTAAAEADSVLNGSPSWH 54
| | : : : : : | | | | : : : : : | | | | : : : : :
| | : : : : : | | | | : : : : : | | | | : : : : :
OY 60 -PGC-----RLAEVCTVLLRLGDELQIRPSYRNVARQLHIPLQ 99
| | : : : : : | | | | : : : : : | | | | : : : : :
| | : : : : : | | | | : : : : : | | | | : : : : :
DB 55 PRAGHVNVGATVHRSSLEVEHIVRASDVROALDADDEFLRYRAFSVDTLSLH--T 111
| | : : : : : | | | | : : : : : | | | | : : : : :
| | : : : : : | | | | : : : : : | | | | : : : : :
OY 100 EPVYTDAPLAAGHIFSGITWGVSLYSVAAGLANDCVRQAPAMVHALVDCLEFEV 159
| | : : : : : | | | | : : : : : | | | | : : : : :
| | : : : : : | | | | : : : : : | | | | : : : : :
DB 112 PGTAYSFEEVVAWELFDHGDGMGRIVAFSFGALCVESYDKRMRLVGRIVSMWTTIYL 171
| | : : : : : | | | | : : : : : | | | | : : : : :
| | : : : : : | | | | : : : : : | | | | : : : : :
OY 160 KTLATWLRRCGW 172
| | : : : : : | | | | : : : : : | | | | : : : : :
| | : : : : : | | | | : : : : : | | | | : : : : :
DB 172 DHLDPMIENGW 184
| | : : : : : | | | | : : : : : | | | | : : : : :
| | : : : : : | | | | : : : : : | | | | : : : : :

RESULT 15
ARL1.XENLA STANDARD: PRT; 204 AA.
ID ARL1.XENLA

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AC O91828;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2 (XRL1).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=83355;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue-Head;
RX MEDLINE=95331613; PubMed=7607538;
RA Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
RL cell-survival genes.";
RL Gene 158:171-179(1995).
CC -! FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
CC -! SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -! DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND
CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC -! SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -! SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -! SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL: X82461; CAA57844.1; -
DR HSP: Q07817; 1MAZ.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR003093; BCL2_BH4.
DR InterPro: IPR004725; BCL2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfam: TIGR00865; bcl-2; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR Apoptosis; Transmembrane.
KW DOMAIN
FT DOMAIN 101 120 BH1.
FT DOMAIN 152 167 BH2.
FT TRANSMEM 181 198 POTENTIAL.
SQ SEQUENCE 204 AA; 23379 MM; 3BFC6BE6DACA03 CRC64;

Query Match 12.8%; Score 139.5; DB 1; Length 204;
Best Local Similarity 26.2%; Pred. No. 1.2e-05;
Matches 28; Conservative 22; Mismatches 54; Indels 3; Gaps 1;

QY 66 EVCYVLRIGDLEQIRSVYRNVARQLHIPLOSEPVTDAFLAVAGHIFSAGITWKKV 125
DB 57 EVLAQLLEATEEFELRYQRAFSDLISQLHI---TODTAQSQSQYMGELFRGTWGRIV 113
QY 126 SLISVAGLAVDCVRAQAPAMVHALVDCLGFEFVKTLATWLRRGW 172
DB 114 AFFSEGRALCVESANKEMTDLPRIYQWNVYLEHTLPWMQENCGW 160
```

Search completed: April 29, 2003, 11:23:54  
Job time : 9.50783 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:20:36 ; Search time 13.3473 Seconds

(without alignments)  
1534.145 Million cell updates/sec

Title: US-09-682-667-2

Perfect score: 1094

Sequence: 1 MEVLRRSSVFPAEIMDAFDR.....TLCSPGRFLKAAFULLPER 213

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161.5	14.8	227	2 JF0203	apoptosis regulator gene bcl-2 protein
2	161.5	14.8	226	2 I53744	transforming protein
3	157.5	14.4	216	2 B37332	B-cell lymphoma 2
4	156.5	14.3	236	2 JC7383	bcl-2 - rat (fragm
5	156	14.3	236	2 I67432	bcl-x transmembran
6	154.5	14.1	214	2 I49057	bcl-x long - mouse
7	154.5	14.1	233	2 I49056	bcl-x protein - ra
8	153.5	14.0	233	2 S51761	transforming prote
9	153.5	13.9	233	2 A37332	transforming prote
10	152.5	13.8	199	1 TVMSB1	BCL-X-long - rat
11	151.5	13.8	233	2 I67431	apoptosis regula
12	151.5	13.8	233	2 I67431	transforming prote
13	150.5	13.8	233	2 B47537	transforming prote
14	150.5	13.8	239	1 TVHU01	transforming prote
15	149.5	13.7	218	2 B47538	bcl-2-associated p
16	149	13.6	232	2 S24390	transforming prote
17	146.5	13.4	179	2 JC7255	Bax delta protein
18	146.5	13.4	205	1 TVHU01	transforming prote
19	144.5	13.2	192	2 A47538	bcl-2-associated p
20	141.5	12.9	190	2 A47537	apoptosis regula
21	132	12.1	211	2 S56873	Bak protein - huma
22	128.5	11.7	192	2 D47538	bcl-2-associated p
23	127	11.6	211	2 S36875	cdn-2 protein - hu
24	124	11.3	133	2 I53295	bcl-2-associated p
25	121	11.1	350	2 A47476	BCL2 homolog MCL1
26	111.5	10.2	143	2 I38921	bcl-2-associated p
27	106	9.7	154	2 I58194	gene bcl-2 protein
28	93.5	8.5	172	2 I49449	hemopoietic-specif
29	93.5	8.5	115	2 A70990	cardanoyl-phosphat

30	93.5	8.5	1203	2 I55466	N-methyl-D-asparta
31	92.5	8.5	175	2 I39055	Bcl-2 related - hu
32	90.5	8.3	118	2 S70089	kora protein - hu
33	88.5	8.1	411	2 E70667	hypothetical prote
34	88	8.0	373	2 H84404	ferichrome ABC tr
35	85.5	7.8	255	2 JC7567	Mcl-1a protein - z
36	85.5	7.8	297	2 B98172	pca operon transcr
37	85.5	7.8	600	2 D87232	conserved membrane
38	84.5	7.7	404	2 E83561	probable type II s
39	84.5	7.7	526	2 B87598	TPR domain protein
40	84.5	7.7	672	2 S46276	acetate-CoA ligase
41	84.5	7.7	1129	2 H86595	probable carbamoyl
42	84	7.7	177	2 S54778	NR-13 protein - qu
43	82.5	7.5	255	2 JC4319	uroporphyrin-III C
44	82.5	7.5	860	2 C83750	manosyltransferas
45	82	7.5	552	2 S71811	probable transcrip

#### ALIGNMENTS

##### RESULT 1

JF0203

apoptosis regulator bcl-x isoform - human

N:Alternate names: h-bcl-xbeta

C:Species: Homo sapiens (man)

C>Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 16-Jul-1999

C:Accession: JF0203

R:Ban, J.; Eckhart, L.; Weninger, W.; Milder, M.; Tschachler, E.

Biochem. Biophys. Res. Commun. 248, 147-152, 1998

A:Title: Identification of a human cDNA encoding a novel bcl-x isoform.

A:Reference number: JF0203; MUID:98340865; PMID:9675101

A:Accession: JF0203

A:Molecule type: mRNA

A:Residues: 1-227 <BAN>

A:Cross-References: GB:U72398; NID:G1622940; PIDN:AB17354.1; PID:G1622941

C:Genetics:

A:Gene: bcl-x

A:Map position: 20

C:Superfamily: bcl transforming protein

##### Query Match

Best Local Similarity 23.7%; Pred. No. 2.1e-07;

Matches 51; Conservative 29; Mismatches 78; Indels 57; Gaps 6;

QY	21	SPIDKELVAQAKRLGREYVHARLRAGLSMS-----APERA-----	56
DB	2	SOSNRELVV-----DFLSYKLSQKGYMSQFSQDVEENRTPEAEGTESEMETPSAINGN	54
QY	57	-----SPAPGGR-----LAEVCTVLLRLGDELEQIRPSYRNVARQLHI	95
DB	55	PSMHLADSPAVNGATGHSLSLARREYIPMAAVQALREAGDEELRYRRAFSDLTSLQHLI	114
QY	96	PIQSEPVVTDALFVAGHIFPSAGITGWKVSLSVSAAGLAVDCVROAPAMVHALVDCIG	155
DB	115	---TPGTAVQSEQVYVNELEFRDGVNNGRIYAFPSFGALCVESVDKEMQVLVSRIAMMA	171
QY	156	EFVAKRLATWLRRGGM--TDVLKCVVSTDPGRS	188
DB	172	TYLNDHLEPWIQENGWVRKPLVCPFSLASGORS	206

##### RESULT 2

I53744

gene bcl-2 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 16-Jul-1999

C:Accession: I53744

R:Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.

Gene 140, 291-292, 1994

A:Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.

A:Reference number: I53744; MUID:94193015; PMID:8144041

A:Accession: I53744

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-236 <RES>  
A:Cross-references: GB:L14680; NID:9408946; PID:AAA53662.1; PID:9408947  
C:Genetics:  
A:Gene: bcl-2  
C:Superfamily: bcl transforming protein

Query Match 14.8%; Score 161.5; DB 2; Length 236;  
Best Local Similarity 23.3%; Pred. No. 2.2e-07;  
Matches 52; Conservative 34; Mismatches 80; Indels 57; Gaps 8;

28 VAQAKALG-----REYHARLLRAGLSM-----SAPERASPAG----- 61  
1 MAQAGTGYDNRREIYWKYIHYKLSQRYEMDGDGDSAPLRAPTPGIRSFQPSNRTPA 60  
62 -----GRLAECYVLLRLGDELEQIRPSYRNVAR-----QLHI-P 96  
61 VHRDPAARTSPRLPIVANAGPALSPVPVHLLTRAGDDFSRRYRDRDAEMSSQLHLTP 120  
97 LOSEPVTDAFLAVAGHIFSAGITWGKVSLSVAAGLAVDCVROQAPAMVHALVDCGEE 156  
121 FTAR-----GRFATVVEELFRDGVNMGRIVAFEEFGVCMCVSVNREMSPLVDNIALMTE 176  
157 EVRKLTATLWLRRRGGWTDVLCVCV-VSTDGFRSHML-VATLCS 197  
177 YLNRHLHTWIQDNGWDADFVELYGPSPRLFPFSWLSLTKLTL 219

RESULT 3  
B37332  
transforming protein (bcl-2-beta) - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 24-Apr-1998  
C:Accession: B37332; S35452  
R:Aguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992  
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues  
A:Reference number: A37332; MUID:92275724; PMID:1508712  
A:Accession: B37332  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-216 <EGU>  
A:Cross-references: EMBL:D11381; EMBL:D11382  
C:Superfamily: bcl transforming protein

Query Match 14.4%; Score 157.5; DB 2; Length 216;  
Best Local Similarity 21.0%; Pred. No. 4.7e-07;  
Matches 45; Conservative 35; Mismatches 77; Indels 57; Gaps 6;

20 RSPDKELVAQAKALGREYVHARLLRAGLSMSA-----PERASPAGGLAEVCT----- 69  
7 KGYDNREIVL-----KTIHYKLSQRYEMDGDGDSAPLRAPTPAAMVAAAGASS 59  
70 -----VLLRLGDELEQIRPSYRNVARQLHI-PIQ 98  
60 HHRPPGSAASEVPAPEGLRPPGVHLLRQAGDSRRYQRFQMSQHLHTLPT 119  
99 SEPVTDAFLAVAGHIFSAGITWGKVSLSVAAGLAVDCVROQAPAMVHALVDCGEE 158  
120 AH-----GRFVAVVEELFRDGVNMGRIVAFEEFGVCMCVSVNREMSPLVDNIALMTE 175  
159 RKTATLWLRRRGGWTDVLCVCVSTDPGFRSHMLV 192  
176 NRHLHTWIQDNGWDADFVELYGPSPRLFPFSWLSLTKLTL 204

RESULT 4  
JC7383  
B-cell lymphoma 2 protein - Chinese hamster  
C:Species: Cricetus griseus (Chinese hamster)  
C:Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 08-Dec-2000  
C:Accession: JC7383

R:Tomlić, M.T.; Christmann, M.; Kaina, B.  
Biochem. Biophys. Res. Commun. 275, 899-903, 2000  
A:Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.  
A:Reference number: JC7383  
A:Contents: Ovary  
A:Accession: JC7383  
A:Molecule type: mRNA  
A:Residues: 1-236 <TOM>  
A:Cross-references: GB:AJ271720  
C:Comment: This protein has anti-apoptotic function, and supports cell survival.  
C:Genetics:  
A:Gene: bcl-2  
C:Superfamily: bcl transforming protein  
C:Keywords: B-cell lymphoma; ovary

Query Match 14.3%; Score 156.5; DB 2; Length 236;  
Best Local Similarity 22.4%; Pred. No. 6.5e-07;  
Matches 50; Conservative 36; Mismatches 80; Indels 57; Gaps 8;

28 VAQAKALG-----REYHARLLRAGLSM-----SAPERASPAG----- 61  
1 MAQAGTGYDNRREIYWKYIHYKLSQRYEMDGDGDSAPLRAPTPGIRSFQPSNRTPA 60  
62 -----GRLAECYVLLRLGDELEQIRPSYRNVAR-----QLHI-P 96  
61 VHRDPAARTSPRLPIVATTPGIRSFQPSNRTPA 120  
97 LOSEPVTDAFLAVAGHIFSAGITWGKVSLSVAAGLAVDCVROQAPAMVHALVDCGEE 156  
121 FTAR-----GRFATVVEELFRDGVNMGRIVAFEEFGVCMCVSVNREMSPLVDNIALMTE 176  
157 EVRKLTATLWLRRRGGWTDVLCVCV-VSTDGFRSHML-VATLCS 197  
177 YLNRHLHTWIQDNGWDADFVELYGPSPRLFPFSWLSLTKLTL 219

RESULT 5  
B67432  
BCL-2 - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Jul-1999  
C:Accession: B67432  
R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.  
Endocrinology 136, 232-241, 1995  
A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: evidence for a role in the regulation of granulosa cell apoptosis  
A:Reference number: B67432  
A:Accession: B67432  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-236 <RES>  
A:Cross-references: EMBL:U34964; NID:91004378; PID:AAA77687.1; PID:91004379  
C:Superfamily: bcl transforming protein

Query Match 14.3%; Score 156; DB 2; Length 236;  
Best Local Similarity 21.5%; Pred. No. 7.2e-07;  
Matches 51; Conservative 36; Mismatches 84; Indels 66; Gaps 8;

28 VAQAKALG-----REYHARLLRAGLSM-----SAPERASPAG----- 61  
1 MAQAGTGYDNRREIYWKYIHYKLSQRYEMDGDGDSAPLRAPTPGIRSFQPSNRTPA 60  
62 -----GRLAECYVLLRLGDELEQIRPSYRNVAR-----QLHI-P 96  
61 VHRDPAARTSPRLPIVANAGPALSPVPVHLLTRAGDDFSRRYRDRDAEMSSQLHLTP 120  
97 LOSEPVTDAFLAVAGHIFSAGITWGKVSLSVAAGLAVDCVROQAPAMVHALVDCGEE 156  
121 FTAR-----GRFATVVEELFRDGVNMGRIVAFEEFGVCMCVSVNREMSPLVDNIALMTE 176  
157 EVRKLTATLWLRRRGGWTDVLCVCV-VSTDGFRSHML-VATLCS 197  
177 YLNRHLHTWIQDNGWDADFVELYGPSPRLFPFSWLSLTKLTL 233











GenCore version 5.1.4 p5.4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:16:46 ; Search time 32.539 Seconds  
(without alignments)  
872.393 Million cell updates/sec

Title: US-09-682-667-2  
Perfect score: 1094  
Sequence: 1 MEVLRRSSVFPAEIMDAEDR.....TLCSPGRFLKAAFFLLPER 213

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.GeneSeq\_101002.\*  
1: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1980.DAT:\*  
2: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT:\*  
3: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1982.DAT:\*  
4: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1983.DAT:\*  
5: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1984.DAT:\*  
6: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1985.DAT:\*  
7: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1986.DAT:\*  
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9: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1988.DAT:\*  
10: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1989.DAT:\*  
11: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1990.DAT:\*  
12: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1991.DAT:\*  
13: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1992.DAT:\*  
14: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1993.DAT:\*  
15: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1994.DAT:\*  
16: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1995.DAT:\*  
17: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1996.DAT:\*  
18: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1997.DAT:\*  
19: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1998.DAT:\*  
20: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA1999.DAT:\*  
21: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:\*  
22: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:\*  
23: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1094	100.0	213	20	AAV14153
2	1076	98.4	213	20	AAV14155
3	1052	96.2	213	21	AAW41444
4	839.5	76.7	170	20	AAV14154
5	828.5	75.7	170	20	AAV14156
6	727	66.5	176	21	AAW58949
7	671	61.3	134	22	AAW58655
8	244.5	22.3	846	22	AAW64401
9	234	21.4	247	22	AAW63760
10	159	14.5	235	19	AAW48312

11	158	14.4	485	22	AAU00222
12	156.5	14.3	239	22	AAW48288
13	156.5	14.3	239	22	AAW50537
14	155.5	14.2	233	22	AAW73304
15	155	14.2	232	22	AAW01020
16	155	14.2	232	20	AAW94347
17	154.5	14.1	233	22	AAW73303
18	154.5	14.1	236	20	AAW87811
19	154.5	14.1	236	22	AAW74128
20	154.5	14.1	236	22	AAW35131
21	154.5	14.1	236	22	AAW76554
22	154.5	14.1	239	22	AAW64037
23	152.5	13.9	221	18	AAW10688
24	152.5	13.9	239	17	AAW02383
25	152.5	13.9	239	22	AAW64036
26	152.5	13.9	239	22	AAW64038
27	152	13.9	239	21	AAW63203
28	151.5	13.8	239	9	AAW80987
29	151.5	13.8	239	14	AAW42312
30	151.5	13.8	239	16	AAW70331
31	151.5	13.8	239	16	AAW71404
32	151.5	13.8	239	17	AAW01018
33	151.5	13.8	239	19	AAW40217
34	151.5	13.8	239	20	AAW94345
35	151.5	13.8	239	20	AAW87812
36	151.5	13.8	239	22	AAE08573
37	151.5	13.8	239	22	AAW64035
38	151.5	13.8	239	22	AAW74129
39	151.5	13.8	239	22	AAW75986
40	151.5	13.8	239	23	AAW05227
41	151.5	13.8	272	19	AAV21120
42	150.5	13.8	233	16	AAW68887
43	150.5	13.8	233	17	AAW05821
44	150.5	13.8	233	18	AAW31530
45	150.5	13.8	233	21	AAW83223

## ALIGNMENTS

RESULT 1	AAV14153	standard; Protein: 213 AA.
ID	AAV14153	
XX	XX	
AC	AAV14153;	
XX	XX	
DT	27-JUL-1999	(first entry)
XX	XX	
DE	Rat Bok protein sequence.	
XX	XX	
KW	Bok protein; Bcl-2-related ovarian killer; BH31 variant; endometriosis;	
KW	pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;	
KW	reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;	
KW	ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;	
XX	XX	
OS	Rattus rattus.	
XX	XX	
PN	W09924453-A1.	
PD	20-MAY-1999.	
XX	XX	
PF	04-NOV-1998;	98WO-US23523.
XX	XX	
PR	07-NOV-1997;	97US-0064943.
XX	XX	
PA	(STRD ) UNIV LELAND STANFORD JUNIOR.	
XX	XX	
PI	Hsu SY, Hsueh AJW;	
XX	XX	
DR	WPI: 1999-327356/27.	
XX	XX	
DR	N-PSDB; AAW61103.	
XX	XX	

LEF-Bcl-XL apoptos  
Human Bcl-2 protei  
Human Bcl-2 protei  
Mutant rat Bcl-XL  
Apoptosis-blocking  
Human Bcl-2 mutant  
Rat wild-type Bcl-  
A murine Bcl-2 pro  
Murine bcl-2. Mus  
Murine Bcl-2. Mus  
Murine Bcl-2 polyP  
Human Bcl-2 protei  
Bax omega protein,  
Human Bcl2. Homo  
Human Bcl-2 protei  
Human Bcl-2 protei  
Amino acid sequenc  
Sequence of bcl-2-  
Bcl-2 oncogene pro  
Human bcl-2 protei  
Human bcl-2 alpha  
Apoptosis-blocking  
Human bcl-2. Homo  
Human Bcl-2 wild-t  
A human Bcl-2-alph  
Human Bcl-2 protei  
Human Bcl-2 protei  
Human bcl-2alpha.  
Protein sequence.  
Human D34A caspase  
Human bcl2 proto-o  
Human thymus BCL-X  
Bcl-XL protein. H  
Human anti-apoptot  
Bcl-x polypeptide.

PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
PI protein and its related gene

PS Claim 2; Page 53-54; 62pp; English.

CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
CC protein, of the invention. Coding sequences for Bok or Bhl3 variants of  
CC pro-apoptotic Bok-related protein can be introduced into cell populations  
CC to upregulate expression of the proteins in order to induce apoptosis in  
CC the cell population. This is useful for treatment of diseases where there  
CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
CC other tissues, and provide a means for manipulating apoptosis. The Bok  
CC protein and transgenic animal are also useful for identifying ligands or  
CC substrates. Modulation of the gene activity in vivo is useful for  
CC prophylaxis and therapy of, e.g. cancer and other proliferative  
CC disorders. Bok genes are also useful for identification of cell type  
CC based on expression. Identification of Bok as a new pro-apoptotic protein  
CC with wide tissue distribution and heterodimerisation properties  
CC facilitates elucidation of apoptosis mechanisms.

CC Sequence 213 AA;

Query Match 100.0%; Score 1094; DB 20; Length 213;

Best Local Similarity 100.0%; Pred. No. 3.6e-111;

Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEVLRSSVFAEIMDADRSPDKELVAQAKALGREYVHARLLRAGLSMSAPERASAP 60

DB 1 MEVLRSSVFAEIMDADRSPDKELVAQAKALGREYVHARLLRAGLSMSAPERASAP 60

QY 61 GGRLAECVTLRLDDELQIRPSYRNVARQLHPILOSEPVYDPAFLAVAGHIFSAGIT 120

DB 61 GGRLAECVTLRLDDELQIRPSYRNVARQLHPILOSEPVYDPAFLAVAGHIFSAGIT 120

QY 121 WGVVSLYSVAAGLAVDCVROAPAMVHALVDCGEEFVKTLATWLRRRGWTDVLCVV 180

DB 121 WGVVSLYSVAAGLAVDCVROAPAMVHALVDCGEEFVKTLATWLRRRGWTDVLCVV 180

QY 181 STDGFRSHMLVATLCSPGRFLKAFLLPPER 213

DB 181 STDGFRSHMLVATLCSPGRFLKAFLLPPER 213

RESULT 2  
ID AAY14155 standard; Protein: 213 AA.

AC AAY14155;

DT 27-JUL-1999 (first entry)

DE Human Bok protein sequence.

KW Bok protein; Bcl-2-related ovarian killer; Bhl3 variant; endometriosis;  
KW pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
KW reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
KW ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
KW proliferative disorder; human.

XX Homo sapiens.

XX OS

XX PN MO9924453-A1.

XX PD 20-MAY-1999.

XX PF 04-NOV-1998; 98WO-US23523.

XX PR 07-NOV-1997; 97US-0064943.

PA (STED ) UNIV LELAND STANFORD JUNIOR.

XX Hsu SY, Hsueh AJW;

XX WPI: 1999-327356/27.

DR N-PSDB: AAX61105.

PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
PI protein and its related gene

PS Claim 2; Page 55-56; 62pp; English.

CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
CC protein, of the invention. Coding sequences for Bok or Bhl3 variants of  
CC pro-apoptotic Bok-related protein can be introduced into cell populations  
CC to upregulate expression of the proteins in order to induce apoptosis in  
CC the cell population. This is useful for treatment of diseases where there  
CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
CC other tissues, and provide a means for manipulating apoptosis. The Bok  
CC protein and transgenic animal are also useful for identifying ligands or  
CC substrates. Modulation of the gene activity in vivo is useful for  
CC prophylaxis and therapy of, e.g. cancer and other proliferative  
CC disorders. Bok genes are also useful for identification of cell type  
CC based on expression. Identification of Bok as a new pro-apoptotic protein  
CC with wide tissue distribution and heterodimerisation properties  
CC facilitates elucidation of apoptosis mechanisms.

CC Sequence 213 AA;

Query Match 98.4%; Score 1076; DB 20; Length 213;

Best Local Similarity 98.6%; Pred. No. 3.3e-109;

Matches 210; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEVLRSSVFAEIMDADRSPDKELVAQAKALGREYVHARLLRAGLSMSAPERASAP 60

DB 1 MEVLRSSVFAEIMDADRSPDKELVAQAKALGREYVHARLLRAGLSMSAPERASAP 60

QY 61 GGRLAECVTLRLDDELQIRPSYRNVARQLHPILOSEPVYDPAFLAVAGHIFSAGIT 120

DB 61 GGRLAECVTLRLDDELQIRPSYRNVARQLHPILOSEPVYDPAFLAVAGHIFSAGIT 120

QY 121 WGVVSLYSVAAGLAVDCVROAPAMVHALVDCGEEFVKTLATWLRRRGWTDVLCVV 180

DB 121 WGVVSLYSVAAGLAVDCVROAPAMVHALVDCGEEFVKTLATWLRRRGWTDVLCVV 180

QY 181 STDGFRSHMLVATLCSPGRFLKAFLLPPER 213

DB 181 STDGFRSHMLVATLCSPGRFLKAFLLPPER 213

RESULT 3  
ID AAB41444 standard; Protein: 213 AA.

AC AAB41444;

DT 08-FEB-2001 (first entry)

DE Human ORFX ORF1208 polypeptide sequence SEQ ID NO:2416.

KW Human; open reading frame; ORFX; detection; cytosolic; hepatotropic;  
KW vulnerrary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;  
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
KW immunostimulant; thymopoietic; coagulant; vasotropic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antinflammatory;  
KW antiviral; antibacterial; antifungal; antihemetic; antithyroid;  
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;



Db 61 GGRLAEVCTVLLRL-----GIT 77

Qy 121 MGKVVSLYSVAAGLAVDCVROAPAMVHALVDCLGEFVKRTLATWLRRGWTDVLCVY 180  
|||||  
Db 78 MGKVVSLYSVAAGLAVDCVROAPAMVHALVDCLGEFVKRTLATWLRRGWTDVLCVY 137  
|||||

Qy 181 STDGFRSHMLVATLCSFGRFLLKAAFFLLPER 213  
|||||  
Db 138 STDGFRSHMLVATLCSFGRFLLKAAFFLLPER 170  
|||||

RESULT 5  
AAY14156  
ID AAY14156 standard; Protein; 170 AA.  
XX  
AC AAY14156;  
XX  
DT 27-JUL-1999 (first entry)  
XX  
DE Human Bok protein sequence.  
XX  
KW Bok protein; Bcl-2-related ovarian killer; BH3 variant; endometriosis;  
KM pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
KM reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
KM ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
KM proliferative disorder; human.  
XX  
OS Homo sapiens.  
XX  
PN WO924453-A1.  
XX  
PD 20-MAY-1999.  
XX  
PF 04-NOV-1998; 98WO-US23523.  
XX  
PR 07-NOV-1997; 97US-0064943.  
XX  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX  
PI Hsu SY, Hsueh AW;  
XX  
DR WPI; 1999-327356/27.  
XX  
DR N-PSDB; AAX61106.  
XX  
PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
PR protein and its related gene  
XX  
PS Claim 2; Page 57-58; 62pp; English.  
XX  
CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
CC pro-apoptotic Bok-related protein can be introduced into cell populations  
CC to upregulate expression of the proteins in order to induce apoptosis in  
CC the cell population. This is useful for treatment of diseases where there  
CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
CC other tissues, and provide a means for manipulating apoptosis. The Bok  
CC protein and transgenic animal are also useful for identifying ligands or  
CC substrates. Modulation of the gene activity in vivo is useful for  
CC prophylaxis and therapy of, e.g. cancer and other proliferative  
CC disorders. Bok genes are also useful for identification of cell type  
CC based on expression. Identification of Bok as a new pro-apoptotic protein  
CC with wide tissue distribution and heterodimerisation properties  
CC facilitates elucidation of apoptosis mechanisms.  
XX  
SQ Sequence 170 AA;

Query Match 75.7%; Score 828.5; DB 20; Length 170;  
Best Local Similarity 78.4%; Pred. No. 2.7e-82;  
Matches 167; Conservative 0; Mismatches 3; Indels 43; Gaps 1;

Qy 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAKALGREYVHARLRAGLSWSPERASPAP 60  
|||||  
Db 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAKALGREYVHARLRAGLSWSPERASPAP 60  
|||||

Qy 61 GGRLAEVCTVLLRLDGELEQIRPSVRYNNARQLHTLPQSEPVYTDALFVAQHSAGIT 120  
|||||  
Db 61 GGRLAEVCTVLLRL-----GIT 77  
|||||

Qy 121 MGKVVSLYSVAAGLAVDCVROAPAMVHALVDCLGEFVKRTLATWLRRGWTDVLCVY 180  
|||||  
Db 78 MGKVVSLYSVAAGLAVDCVROAPAMVHALVDCLGEFVKRTLATWLRRGWTDVLCVY 137  
|||||

Qy 181 STDGFRSHMLVATLCSFGRFLLKAAFFLLPER 213  
|||||  
Db 138 STDGFRSHMLVATLCSFGRFLLKAAFFLLPER 170  
|||||

RESULT 6  
AAB58949  
ID AAB58949 standard; Protein; 176 AA.  
XX  
AC AAB58949;  
XX  
DT 27-MAR-2001 (first entry)  
XX  
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 657.  
XX  
KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;  
KM neotropic; neuroprotective; antiviral; anti-allergic; hepatotropic;  
KM anti-diabetic; anti-inflammatory; antitumor; vulnerability; anticonvulsant;  
KM antibacterial; antifungal; antiparasitic; cardiant; immune disorder;  
KM Addison's disease; allergy; autoimmune hemolytic anaemia;  
KM autoimmune thyroiditis; diabetes mellitus; Crohn's disease;  
KM multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
KM cardiovascular disorder; wound healing; neurological disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200055173-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 08-MAR-2000; 2000WO-US05881.  
XX  
PR 12-MAR-1999; 99US-0124270.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
DR WPI; 2000-611515/58.  
XX  
DR N-PSDB; AAF21852.  
XX  
PT New human breast and ovarian cancer associated gene sequences and the  
PR polypeptides encoded by these genes, useful in the prevention,  
PT treatment and diagnosis of cancer. Immune disorders, cardiovascular  
PT disorders and neurological diseases -  
XX  
PS Claim 11; Page 1103; 1299pp; English.  
XX  
CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human  
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are  
CC associated with breast and ovarian cancer. Included in the invention are  
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the  
CC isolation and characterisation of the DNA and protein sequences of the  
CC invention. The breast and ovarian cancer associated DNA, protein, agonist  
CC or antagonist sequences exhibit cytostatic; immunosuppressive;  
CC neotropic; neuroprotective; antiviral; anti-allergic; hepatotropic;  
CC anti-diabetic; anti-inflammatory; antitumor; vulnerability; anticonvulsant;  
CC antibacterial; antifungal; antiparasitic and cardiant activity. The  
CC polynucleotide and protein sequences are used in the diagnosis of cancer,  
CC particularly breast and ovarian cancer. The nucleic acid sequences,

CC proteins, agonists and agonists may also be used in the diagnosis,  
 CC prevention and treatment of immune disorders e.g. Addison's disease,  
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,  
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid  
 CC arthritis and ulcerative colitis; cardiovascular disorders such as  
 CC myocardial ischaemia; wound healing; neurological diseases such as  
 CC cerebral anoxia and epilepsy; and infectious diseases.

CC Sequence 176 AA:

Query Match 66.5%; Score 727; DB 21; Length 176;

Best Local Similarity 90.1%; Pred. No. 3.4e-71;

Matches 145; Conservative 3; Mismatches 9; Indels 4; Gaps 2;

OY 55 RASPAGGRLAECYCT--VLLRLGDELEJOIRPSYRNVAROLHPLQSEPVYTDALFVAVG 112  
 DB 18 RFSGSG--LXERGTSAVILRLGDELEMTIRPSYRNVAQOLHISLOSEPVYTDALFVAVG 75  
 OY 113 HIFSAGITWGVVSLXSVAGLAVDCVROAPAMVHALVDCGFEVVKTLATWLRRRGGM 172  
 DB 76 HIFSAGITWGVVSLXSVAGLAVDCVROAPAMVHALVDCGFEVVKTLATWLRRRGGM 135  
 OY 173 TDVLCVSTDPGFRSHMLVATLCSGRFLKAAFFLLPER 213  
 DB 136 TDVLCVSTDPGFRSHMLVATLCSGRFLKAAFFLLPER 176

RESULT 7

ABB85665

ID AAB85665 standard; Protein: 134 AA.

XX AAB85665;

DF 29-OCT-2001 (first entry)

DE Human Bcl-2-like polypeptide (clone HHEF17).

KM Bcl-2-like polypeptide; autoimmune disorder; allergy; immunomodulatory;  
 KW respiratory; cardiovascular; antiarthritic; immunostimulant; vaccine;  
 KW immunosuppressive; antiinflammatory; gene therapy.

OS Homo sapiens.

PN WO200157060-A1.

PD 09-AUG-2001.

PF 31-JAN-2001; 2001WO-US03080.

PR 01-FEB-2000; 2000US-0179487.

PR 07-FEB-2000; 2000US-0180697.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Duan DR, Ni J;

DR WPI: 2001-476279/51.

DR N-PSDB: AAH47021.

PT Nucleic acids encoding human Bcl-2-like polypeptides, useful for  
 PT preventing, diagnosing and/or treating -

PS Claim 12; Page 277-278; 285pp; English.

XX The invention provides nucleic acid molecules (NMI) encoding a human  
 CC Bcl-2-like polypeptides (PEP1). The NMI and PEP1 may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate Bcl-2-like polypeptides' expression. The NMI may be used  
 CC to produce the soluble Bcl-2-like polypeptides by standard recombinant  
 CC methodology. The polypeptides may also be used as antigens in the  
 CC production of antibodies against Bcl-2 and in assays to identify  
 CC modulators of Bcl-2 expression and activity. The anti-Bcl-2 antibodies  
 CC and antagonists may be used to down regulate expression and activity.

CC The anti-PEP1 antibodies may also be used as diagnostic agents for  
 CC detecting the presence of Bcl-2 polyps in samples (e.g. by enzyme linked  
 CC immunosorbent assay (ELISA)). Disorders that may be prevented, diagnosed  
 CC and/or treated by the above methods include, immunodeficiencies (e.g.  
 CC a gammaglobulinemia and B cell lymphoproliferative disorder), autoimmune  
 CC disorders (e.g. rheumatoid arthritis and Grave's disease), allergic  
 CC reactions, inflammations, respiratory diseases and cardiovascular  
 CC disorders (a full list of disorders is given in the specification). The  
 CC present sequence represents a human Bcl-2-like polypeptide.

CC Sequence 134 AA:

Query Match 61.3%; Score 671; DB 22; Length 134;

Best Local Similarity 96.2%; Pred. No. 3.1e-65; Matches 128; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 81 IRPSYRNVAROLHPLQSEPVYTDALFVAVGHIFSAGITWGVVSLXSVAGLAVDCVR 140  
 DB 2 IRPSYRNVAROLHISLOSEPVYTDALFVAVGHIFSAGITWGVVSLXSVAGLAVDCVR 61  
 OY 141 QAPAMVHALVDCGFEVVKTLATWLRRRGGMVDVLCVSTDPGFRSHMLVATLCSFGR 200  
 DB 62 QAPAMVHALVDCGFEVVKTLATWLRRRGGMVDVLCVSTDPGFRSHMLVATLCSFGR 121  
 OY 201 FLKAAFFLLPER 213  
 DB 122 FLKAAFFLLPER 134

RESULT 8

ABB64401

ID ABB64401 standard; Protein: 846 AA.

XX ABB64401;

DF 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 19995.

KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE ) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI: 2001-656860/75.

DR N-PSDB: ABL08504.

PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -

PS Disclosure: SEQ ID NO 19995; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins

CC (ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
CC  
XX  
SQ Sequence 846 AA:  
Query Match 22.3%; Score 244.5; DB 22; Length 846;  
Best Local Similarity 35.9%; Pred. No. 1.3e-17;  
Matches 56; Conservative 27; Mismatches 64; Indels 9; Gaps 4;  
QY 26 ELVAQAKALGREYVHARLLRAG-LSMSAPER----ASPAFGRLAECVLLRLDGELEQ 80  
Db 96 DIINGCKCICGQYIRARLRAGVLRNKKYQRLNLLDPSSHVVEVFPALNSMGEELER 155  
QY 81 IRPSYRVNAROL-HIP--LQSEPVYTDAPFLAVAGHIFSAGITGKVSLSVAAGLAV 136  
Db 156 MHPRYTINSRSLRAFPELESDMAPRLNLVAKDLFRSSITWCKIISITFVCGGFAI 215  
QY 137 DCVROAOPAMVHALVDCLGEEYVKTLATWLRRCGW 172  
Db 216 DCVROGHEDYLOCLDGLAEIIEDLLVYWLINDGW 251  
RESULT 9  
ABB63760  
ID ABB63760 standard; Protein; 247 AA.  
XX  
AC ABB63760;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster polypeptide SEQ ID NO 18072.  
XX  
KM Drosophila: developmental biology; cell signalling; insecticide;  
XX  
KN pharmaceutical.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US09231.  
XX  
PR 23-MAR-2000; 2000US-191637P.  
XX  
PR 11-JUL-2000; 2000US-0614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
DR WPI; 2001-656860/75.  
XX  
DR N-PSDB; ABL07863.  
XX  
PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -  
XX  
PS Disclosure; SEQ ID NO 18072; 21pp + Sequence listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins  
CC (ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX

SQ Sequence 247 AA:  
Query Match 21.4%; Score 234; DB 22; Length 247;  
Best Local Similarity 33.3%; Pred. No. 3.6e-17;  
Matches 54; Conservative 29; Mismatches 61; Indels 18; Gaps 4;  
QY 25 KELVAQAKALGREYVHARLLRAGL--SWSAPERASPAPG---GRLAECVLLRLDGELE 78  
Db 87 ODIISGRCLCGHYIKRRLRSGLEPNKKLGIRISILGSTSMGIVRDVFPAYQVLGDEL 146  
QY 79 EDIRPSYRVNAROL-----HIPLOSEPVYTDAPFLAVAGHIFSAGITGKVSLSV 130  
Db 147 ERMHPRIYNGVARQICRNPGEGFHP---DAVSLDLAVAGRELRLVETWSKVISLPAI 202  
QY 131 AAGLAVDCVROAOPAMVHALVDCLGEEYVKTLATWLRRCGW 172  
Db 203 AGSLSDCVROGHEDYLOCLDGLAEIIEDLLVYWLINDGW 244  
RESULT 10  
AAM48312  
ID AAM48312 standard; Protein; 235 AA.  
XX  
AC AAM48312;  
XX  
DT 20-JUL-1998 (first entry)  
XX  
DE Mouse BCL-x gamma.  
XX  
KM BCL-x gamma; mouse; apoptosis; T cell receptor; immunodeficiency;  
KM autoimmune disorder; graft-versus-host disease; diabetes mellitus;  
KM arthritis; multiple sclerosis; myasthenia gravis; dermatitis;  
KM systemic lupus erythematosus; autoimmune thyroiditis; allergy;  
KM psoriasis; Sjogren's syndrome; alopecia areata; Crohn's disease;  
KM aphthous ulcer; lrlitis; conjunctivitis; keratoconjunctivitis;  
KM ulcerative colitis; asthma; cutaneous lupus erythematosus;  
KM scleroderma; vaginitis; proctitis; erythema nodosum leprosum;  
KM leprosy; autoimmune uveitis; allergic encephalomyelitis;  
KM acute necrotising haemorrhagic encephalopathy; anaemia;  
KM idiopathic bilateral progressive sensorineural hearing loss;  
KM thrombocytopenia; polychondritis; Wegener's granulomatosis;  
KM chronic active hepatitis; Stevens-Johnson syndrome; sarcoidosis;  
KM idiopathic sprue; lichen planus; Graves ophthalmopathy;  
KM primary biliary cirrhosis; uveitis posterior; lung fibrosis;  
KM reticular dysgenesis; agammaglobulinaemia; hypogammaglobulinaemia;  
KM Wiskott-Aldrich syndrome; ataxia telangiectasia; DiGeorge syndrome;  
KM Bloom syndrome; Fanconi anaemia; AIDS; therapy; diagnosis.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FH Domain 185..235  
FH /note="gamma domain"  
FH Domain 185..217  
FH /note="ankyrin domain"  
XX  
PN WO9805777-A2.  
XX  
PD 12-FEB-1998.  
XX  
PD 25-JUL-1997; 97WO-US12899.  
XX  
PR 02-AUG-1996; 96US-0023666.  
XX  
PA (DAND ) DANA FARBER CANCER INST INC.  
XX  
PI Cantor H, Weber GF, Yang X;  
XX  
DR WPI; 1998-145613/13.  
XX  
DR N-PSDB; AAV17638.  
XX  
PT BCL-x gamma, a new isoform of the BCL-x family of proteins -  
PT provides resistance to T cell receptor dependent apoptosis, used to



PT develop products for treating autoimmune disorders or  
 PT immunodeficiencies

PS Claim 8; Page 84; 123pp; English.

XX This amino acid sequence comprises mouse BCL-x gamma, a novel,  
 CC isoform of the BCL-x family that has a novel C-terminal gamma  
 CC domain. The sequence was deduced from an isolated cDNA clone  
 CC (see AAV17638) from a thymus cDNA library. n ankyrin domain and which  
 CC is predominantly expressed in T-lymphocytes and which is associated  
 CC with resistance to apoptosis. BCL-x gamma polypeptides can be  
 CC expressed in host cells and used to screen for modulator compounds.  
 CC BCL-x gamma activity can be down-modulated in order to ameliorate  
 CC an autoimmune disorder such as graft-versus-host disease, cases of  
 CC transplantation, and autoimmune diseases e.g. diabetes mellitus,  
 CC arthritis, multiple sclerosis, myasthenia gravis, systemic lupus  
 CC erythematosus, autoimmune thyroiditis, dermatitis, psoriasis,  
 CC Sjogren's syndrome, alopecia areata, allergic responses to  
 CC arthropod bite, Crohn's disease, aphthous ulcer, lrlitis,  
 CC conjunctivitis, keratoconjunctivitis, ulcerative colitis, asthma,  
 CC cutaneous lupus erythematosus, scleroderma, vaginitis, proctitis,  
 CC drug eruptions, leprosy reversal reactions, erythema nodosum leprosum,  
 CC autoimmune uveitis, allergic encephalomyelitis, acute necrotizing  
 CC haemorrhagic encephalopathy, idiopathic bilateral progressive  
 CC sensorineural hearing loss, aplastic anaemia, pure red cell anaemia,  
 CC idiopathic thrombocytopenia, polyorchiditis, Wegener's granulomatosis,  
 CC chronic active hepatitis, Stevens-Johnson syndrome, idiopathic sprue,  
 CC lichen planus, Graves ophthalmopathy, sarcoidosis, primary biliary  
 CC cirrhosis, uveitis posterior, and interstitial lung fibrosis.  
 CC BCL-x gamma activity can be upmodulated, e.g. by gene therapy, to  
 CC ameliorate e.g. severe combined immunodeficiency, adenosine deaminase  
 CC deficiency, purine nucleoside phosphorylase deficiency, MHC class II  
 CC X-linked hypogammaglobulinaemia, Ig deficiency with increased IGM,  
 CC Ig heavy chain-gene deletions, k-chain deficiency Iga deficiency,  
 CC selective deficiency of IgG subclass, common variable  
 CC immunodeficiency, transient hypogammaglobulinaemia of infancy,  
 CC Wiskott-Aldrich syndrome, ataxia telangiectasia, DiGeorge syndrome,  
 CC Bloom syndrome, Fanconi anaemia, and Down syndrome-related  
 CC immunodeficiency, as well as other syndromes associated with  
 CC immunodeficiency and immunodeficiencies resulting from other causes,  
 CC such as HIV disease and AIDS. Additionally, it may be desirable to  
 CC upregulate BCL-x gamma activity to increase T cell survival in the  
 CC case of other disorders, e.g. cellular responses to tumours, or  
 CC pathogens.

XX Sequence 235 AA;

Query Match 14.5%; Score 159; DB 19; Length 235;  
 Best Local Similarity 22.3%; Pred. No. 5, 2e-09;  
 Matches 52; Conservative 31; Mismatches 80; Indels 70; Gaps 8;

OY 21 SPDKELVQAKALGREYHARLRAGLSMS-----APEKA----- 56  
 DB 2 SOSNRELVV-----DFLSYKLSQKGYMSQPSDVENRTEPEETEARPPSAINGN 54  
 OY 57 -----SPAPGR-----LAECVTLLRLGDELEQIRPSYRNVAROLHI 95  
 DB 55 PSMHLADSAVNGATGHSSSLDAREVYIPMAAVKQALREANGDEFLATRRFSLTQLOHI 114  
 OY 96 PLOSEPVYTDALFVAGHIFPSAGITGWKVSLSVAAGLAVDCVROAQPAMVHALVCLIG 155  
 DB 115 ---TPGTAVQSEFOVYVNEFLRDGVNMGRIYAFPSFGALCVESVDKEMQVLSRIASWMA 171  
 OY 156 EPYRKRLAMLRIRGGM-----TDVLKCVSTDPGRFSH-----WLYAT 194  
 DB 172 TYLNDLHPWIDENGWVGSGTPLRSVFRRLVQV--PGVAEHVCDDPSLWEVET 223

RESULT 11  
 AAU00222  
 ID AAU00222 standard; Protein; 485 AA.  
 XX

AC AAU00222;  
 XX 31-MAY-2001 (first entry)

DE LFn-Bcl-XL apoptosis-modifying fusion protein.

KW Human; LFn-Bcl-XL; apoptosis; cancer; spinal muscular atrophy;

KW anthrax lethal factor; neoplasm; tumour; hyper-proliferation;

KW Alzheimer's disease; neurodegenerative disorder; stroke;

KW transient ischaemic neuronal injury; spinal cord injury;

KW Huntington's disease.

OS Chimeric - Homo sapiens.

OS Chimeric - Corynebacterium diptheriae.

OS Chimeric - Synthetic.

FT Key Location/Qualifiers

FT Region 5..10

FT Region /note="6x histidine tag"

FT Region 21..276

FT Region /note="Anthrax lethal factor amino acids 1 to 255"

FT Region 277..485

FT Region /note="Bcl-XL amino acids 1 to 209"

WO200112661-A2.

22-FEB-2001.

15-AUG-2000; 2000MO-US22293.

16-AUG-1999; 99US-0149220.

(HARD ) HARVARD COLLEGE.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

WPI: 2001-218343/22.

N-PSDB; AAS00250.

Youle RJ, Liu X, Collier RJ;

Novel fusion protein for modifying apoptosis in target cell and

reducing apoptosis after transient ischaemic neuronal injury, has two

domains which targets protein to a cell and modifies apoptotic response

of cell

Claim 4; Page 64-65; 65pp; English.

The sequence represents the amino acid sequence of LFn-Bcl-XL apoptosis-modifying fusion protein comprising anthrax lethal factor (LF) sequence fused to Bcl-XL. The functional apoptosis-modifying fusion protein is capable of binding a target cell and integrating into or crossing a cellular membrane of the target cell. The apoptosis-modifying fusion protein comprises at least two domains: the DTR domain, which targets the fusion protein to the target cell and the Bcl-XL domain, which modifies an apoptotic response of the target cell. The fusion protein is useful for modifying (inhibiting or enhancing) apoptosis in a target cell, such as neuron, lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or hyper-proliferative cell or an adipocyte. It is also useful for reducing apoptosis in a subject after transient ischaemic neuronal injury, especially spinal cord injury. The fusion protein may be used to treat various diseases and injury conditions through inhibition or enhancement of apoptotic cellular response, including neurodegenerative disorders such as Alzheimer's disease, Huntington's disease, spinal muscular atrophy, stroke episodes and unregulated cell growth as in tumours and various cancers. The apoptosis-modifying fusion protein can be delivered effectively throughout the body and targeted to selective tissue and cells.

Sequence 485 AA;

Query Match 14.4%; Score 158; DB 22; Length 485;  
 Best Local Similarity 21.8%; Pred. No. 1, 7e-08;  
 Matches 47; Conservative 33; Mismatches 88; Indels 48; Gaps 4;





Db 133 DGVNMGRIVAFEFEGGVMCEVSYNREMSPLVDNIALMTETELNRHLHTWIODNGMDAFV 192  
Qy 177 KCV-VSTDGFRSHWL-VATLCS 197  
Db 193 ELYGPMRPLFDPSMSTLKLIS 215

Search completed: April 29, 2003, 11:23:21  
Job time : 34.5339 secs

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:19:46 ; Search time 21.7493 seconds  
(without alignments)  
1610.532 Million cell updates/sec

Title: US-09-682-667-4

Perfect score: 878

Sequence: 1 MEVLRRSSVFYFAEIMDAFDR.....TLCSGFLKAAFLLLPER 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP RODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_VIRUS:\*  
16: SP\_BACTERIAP:\*  
17: SP\_ARCHAEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	878	100.0	170	11	088857
2	846.5	96.4	213	11	035425
3	828.5	94.4	213	4	090132
4	801	91.2	212	4	090MX3
5	699.5	79.7	213	13	091812
6	693.5	79.0	213	13	09DGJ5
7	183	20.8	299	5	08T8V5
8	183	20.8	313	5	09NGX3
9	173.5	19.8	247	5	09V612
10	173	19.7	300	5	09V9C8
11	142	16.2	317	5	095083
12	126.5	14.4	236	11	0923R6
13	109.5	12.5	192	13	0919N4
14	109.5	12.5	219	11	099N36
15	109.5	12.5	235	11	035843
16	107.5	12.2	238	13	090298

17	105	12.0	180	6	Q9BDD5	Q9bdd5 bos taurus
18	105	12.0	188	11	Q9G0X2	Q9g0x2 mus musculus
19	105	12.0	217	11	Q9GNX3	Q9gnx3 mus musculus
20	105	12.0	233	11	Q35844	Q35844 mus musculus
21	104	11.8	233	6	Q9M257	Q9m257 ovis aries
22	104	11.8	233	6	Q9N1A2	Q9n1a2 sus scrofa
23	103	11.7	180	6	Q9BDX7	Q9bdx7 bos taurus
24	103	11.7	188	4	Q9H1R6	Q9h1r6 homo sapien
25	103	11.7	233	6	Q9MTW4	Q9myw4 cryptotagus
26	103	11.7	233	6	Q8S042	Q8sg42 felis silve
27	100	11.4	163	6	Q9M256	Q9m256 ovis aries
28	100	11.4	193	11	Q88996	Q88996 rattus norv
29	100	11.4	221	13	Q98U13	Q98u13 xenopus lae
30	99	11.3	204	13	Q902H2	Q902h2 xenopus lae
31	98	11.2	178	11	Q9CYW5	Q9cyw5 mus musculus
32	98	11.2	179	4	Q9NKG7	Q9nkg7 homo sapien
33	95	10.8	173	11	Q9UKL3	Q9ukl3 rattus norv
34	94.5	10.8	209	11	Q9UK59	Q9uk59 rattus norv
35	93	10.6	114	4	Q9NR76	Q9nr76 homo sapien
36	93	10.6	149	6	Q9G0G7	Q9g0g7 ovis aries
37	93	10.6	173	4	Q8W249	Q8w249 homo sapien
38	93	10.6	192	6	Q8S043	Q8sg43 felis silve
39	91	10.4	172	11	Q55177	Q55177 mus musculus
40	90.5	10.3	182	16	Q8XUQ3	Q8xug3 raietonia s
41	87.5	10.0	172	11	Q55179	Q55179 mus musculus
42	86	9.8	175	11	Q925A9	Q925a9 rattus norv
43	85	9.7	308	17	Q8TX05	Q8tx05 methanopyru
44	82.5	9.4	412	16	Q9R135	Q9r135 streptomyce
45	80.5	9.2	860	16	Q9PEZ1	Q9pez1 xyella tas

## ALIGNMENTS

RESULT 1  
ID 088857 PRELIMINARY; PRT; 170 AA.  
AC 088857;  
DT 01-NOV-1998 (TREMREL. 08, Created)  
DT 01-NOV-1998 (TREMREL. 08, last sequence update)  
DT 01-JUN-2002 (TREMREL. 21, last annotation update)  
DE Bcl-2-related ovarian killer protein.  
GN BOK.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=OVARY;  
RX MEDLINE=98024143; PubMed=9356461;  
RA Hsu S.Y., Kaipia A., McGee E., Lomeli M., Hsueh A.J.W.;  
RT "Bok is a pro-apoptotic bcl-2 protein with restricted expression in  
reproductive tissues and heterodimerizes with selective anti-apoptotic  
bcl-2 family members.";  
RT Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=OVARY;  
RA Hsu S.Y., Hsueh A.J.W.;  
RT "A splicing variant of the Bcl-2 member Bok with a truncated BH3  
domain induces apoptosis without dimerization with anti-apoptotic Bcl-  
2 proteins.";  
RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF051093; AAC61928.1; -  
DR InterPro: IPR000712; Bcl2\_BH.  
DR InterPro: IPR002475; BCL2\_family.  
DR Pfam: PF00452; Bcl-2; 1.  
DR SMART: SM00337; BCL: 1.  
DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
SQ SEQUENCE 170 AA; 18729 MW; 15E54361F448CF16 CRC64;  
Query Match 100.0%; Score 878; DB 11; Length 170;

Best Local Similarity 100.0%; Pred. No. 1.6e-74;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAALGREYHARLRAGLSMSAPERASAP 60  
DB 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAALGREYHARLRAGLSMSAPERASAP 60  
OY 61 GGRLAECTVLLRLGTTGCKVSVLSVAGLAVDCVROAOPAMVHALVDCIGEFVAKTIA 120  
DB 61 GGRLAECTVLLRLGTTGCKVSVLSVAGLAVDCVROAOPAMVHALVDCIGEFVAKTIA 120  
OY 121 TWLRRGGTVDLKCYSVTDPRGRSHLVATLCSFGRFKAFFLLPPER 170  
DB 121 TWLRRGGTVDLKCYSVTDPRGRSHLVATLCSFGRFKAFFLLPPER 170

## RESULT 2

035425 PRELIMINARY; PRT; 213 AA.

AC 035425;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
DE BCL-2-related ovarian killer protein.  
GN BOK OR BOKL OR BOK OR MTD.  
OS Rattus norvegicus (Rat), and  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;  
OX NCBI\_TaxID=10116, 10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Rat; STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY, TESTIS, AND UTERUS;  
RX MEDLINE=98024143; PubMed=9356461;  
RA Hsu S.Y., Kaipia A., McGee E., Lomeli M., Hsueh A.J.W.;  
RT "Bok is a pro-apoptotic Bcl-2 protein with restricted expression in  
reproductive tissues and heterodimerizes with selective anti-apoptotic  
Bcl-2 family members."  
RL Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Rat; STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY, TESTIS, AND UTERUS;  
RA Hsu S.Y., Hsueh A.J.W.;  
RL Submitted (Oct-1997) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES-Mouse;  
RA Inohara N., Ekhterae D., Garcia I., Carrio R., Merino J., Merry A.,  
Chen S., Nunez G.;  
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF027954; AAB87418.1; -;  
DR EMBL; AF027707; AAC53582.1; -;  
DR MGD; MGI:1858494; Bok.  
DR InterPro: IPR000712; Bcl2\_BH.  
DR InterPro: IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR SMART; SM00337; BCL; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
SQ SEQUENCE 213 AA; 23456 MW; F8755C45CB05D626 CRC64;

Query Match 96.4%; Score 846.5; DB 11; Length 213;  
Best Local Similarity 79.8%; Pred. No. 1.8e-71;  
Matches 170; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

OY 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAALGREYHARLRAGLSMSAPERASAP 60  
DB 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAALGREYHARLRAGLSMSAPERASAP 60  
OY 61 GGRLAECTVLLRLGTTGCKVSVLSVAGLAVDCVROAOPAMVHALVDCIGEFVAKTIA 120  
DB 61 GGRLAECTVLLRLGTTGCKVSVLSVAGLAVDCVROAOPAMVHALVDCIGEFVAKTIA 120  
OY 121 TWLRRGGTVDLKCYSVTDPRGRSHLVATLCSFGRFKAFFLLPPER 170  
DB 121 TWLRRGGTVDLKCYSVTDPRGRSHLVATLCSFGRFKAFFLLPPER 170

DB 121 WCKVSVLSVAGLAVDCVROAOPAMVHALVDCIGEFVAKTIA TWLRRGGTVDLKCIV 180

OY 138 STDPGRSHMLVATLCSFGRFKAFFLLPPER 170  
DB 181 STDPGRSHMLVATLCSFGRFKAFFLLPPER 213

## RESULT 3

09UL32 PRELIMINARY; PRT; 213 AA.

AC 09UL32;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
DE BCL-2 related ovarian killer.  
GN BOK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homd.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hsu S.Y., Hsueh A.J.W.;  
RT "cDNA cloning of the human Bok gene."  
RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF089746; AAF09129.1; -;  
DR InterPro: IPR000712; Bcl2\_BH.  
DR InterPro: IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR SMART; SM00337; BCL; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
SQ SEQUENCE 213 AA; 23540 MW; 59509F8C730517F CRC64;

Query Match 94.4%; Score 828.5; DB 4; Length 213;  
Best Local Similarity 78.4%; Pred. No. 8.6e-70;  
Matches 167; Conservative 0; Mismatches 3; Indels 43; Gaps 1;

OY 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAALGREYHARLRAGLSMSAPERASAP 60  
DB 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAALGREYHARLRAGLSMSAPERASAP 60  
OY 61 GGRLAECTVLLRLGTTGCKVSVLSVAGLAVDCVROAOPAMVHALVDCIGEFVAKTIA 120  
DB 61 GGRLAECTVLLRLGTTGCKVSVLSVAGLAVDCVROAOPAMVHALVDCIGEFVAKTIA 120  
OY 78 WCKVSVLSVAGLAVDCVROAOPAMVHALVDCIGEFVAKTIA TWLRRGGTVDLKCIV 137  
DB 121 WCKVSVLSVAGLAVDCVROAOPAMVHALVDCIGEFVAKTIA TWLRRGGTVDLKCIV 180  
OY 138 STDPGRSHMLVATLCSFGRFKAFFLLPPER 170  
DB 181 STDPGRSHMLVATLCSFGRFKAFFLLPPER 213

## RESULT 4

09UMX3 PRELIMINARY; PRT; 212 AA.

AC 09UMX3;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
DE BCL-2-related ovarian killer protein (Similar to BCL-2-related ovarian  
killer protein-like-PENDING) (BCL-2-related ovarian killer  
protein-like).  
GN BOK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zhang H.;

RT "Gene expression of a human homolog of BCL-2-related ovarian killer protein.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-MUSCLE;  
 RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-MUSCLE;  
 RA Strausberg R.;  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF174487; AAD51719.1; -  
 DR EMBL; BC006203; AA006203.1; -  
 DR EMBL; BC017214; AAH17214.1; -  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; BCL-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 212 AA; 23280 MW; 053ED605FE8E5B2 CRC64;

Query Match 91.2%; Score 801; DB 4; Length 212;  
 Best Local Similarity 76.1%; Pred. No. 3.2e-67;  
 Matches 162; Conservative 3; Mismatches 4; Indels 44; Gaps 2;

QY 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAKALGREYVARLLRAGLSASAPERASAP 60  
 DB 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAKALGREYVARLLRAGLSASAPERASAP 60  
 QY 61 GGRLAECVTVLLRL-----GTF 77  
 DB 61 -GRLAEVCATLLRLGDELEYIRPNVYRNARQLNISLHSEVTYTDALFAVAQIFTAGIT 119  
 QY 78 WGRVSLISYAAGLAADVCAQAPAMVHALVDCGFEVRKTLTWLRRGGMTDYLKCV 137  
 DB 120 WGRVSLISYAAGLAADVCAQAPAMVHALVDCGFEVRKTLTWLRRGGMTDYLKCV 179  
 QY 138 STDPGFRSHWLVAATLCSFGFRFLKAFFLLPER 170  
 DB 180 STDPGFRSHWLVAATLCSFGFRFLKAFFLLPER 212

RESULT 5  
 091812 PRELIMINARY; PRT; 213 AA.  
 ID 091812;  
 AC 091812;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DE Bcl-2-related ovarian killer protein.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20487164; PubMed=11034351;  
 RA Zhang H., Holzgrevé W., De Geyter C.;  
 RL Evolutionarily conserved Bcl proteins in the Bcl-2 family.";  
 RT FEBS Lett. 480:311-313(2000).  
 DR EMBL; AF275944; AAF81282.1; -  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; BCL-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 213 AA; 23619 MW; B3AF7049F25442E3 CRC64;

Query Match 79.7%; Score 699.5; DB 13; Length 213;  
 Best Local Similarity 62.9%; Pred. No. 1e-57;

Matches 134; Conservative 18; Mismatches 18; Indels 43; Gaps 1;

QY 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAKALGREYVARLLRAGLSASAPERASAP 60  
 DB 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAKALGREYVARLLRAGLSASAPERASAP 60  
 QY 61 GGRLAECVTVLLRL-----GTF 77  
 DB 61 GGRLAECVTVLLRLGDELEYIRPNVYRNARQLNISLHSEVTYTDALFAVAQIFTAGIT 120  
 QY 78 WGRVSLISYAAGLAADVCAQAPAMVHALVDCGFEVRKTLTWLRRGGMTDYLKCV 137  
 DB 121 WGRVSLISYAAGLAADVCAQAPAMVHALVDCGFEVRKTLTWLRRGGMTDYLKCV 180  
 QY 138 STDPGFRSHWLVAATLCSFGFRFLKAFFLLPER 170  
 DB 181 STDPGFRSHWLVAATLCSFGFRFLKAFFLLPER 213

RESULT 6  
 09DGJ5 PRELIMINARY; PRT; 213 AA.  
 ID 09DGJ5;  
 AC 09DGJ5;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DE Bcl-2-related ovarian killer protein.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Ellis E.M., Johnson A.L., Bridgman J.T.;  
 RL Characterization and Expression of Bcl in the Hen Ovary.";  
 RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF290888; AAG01182.1; -  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; BCL-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 213 AA; 23658 MW; 07CC06BBD7311EC CRC64;

Query Match 79.0%; Score 693.5; DB 13; Length 213;  
 Best Local Similarity 62.0%; Pred. No. 3.7e-57;  
 Matches 132; Conservative 19; Mismatches 19; Indels 43; Gaps 1;

QY 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAKALGREYVARLLRAGLSASAPERASAP 60  
 DB 1 MEVLRRSSVFAAEIMDAFDRSPTDKELVAQAKALGREYVARLLRAGLSASAPERASAP 60  
 QY 61 GGRLAECVTVLLRL-----GTF 77  
 DB 61 GGRLAECVTVLLRLGDELEYIRPNVYRNARQLNISLHSEVTYTDALFAVAQIFTAGIT 120  
 QY 78 WGRVSLISYAAGLAADVCAQAPAMVHALVDCGFEVRKTLTWLRRGGMTDYLKCV 137  
 DB 121 WGRVSLISYAAGLAADVCAQAPAMVHALVDCGFEVRKTLTWLRRGGMTDYLKCV 180  
 QY 138 STDPGFRSHWLVAATLCSFGFRFLKAFFLLPER 170  
 DB 181 STDPGFRSHWLVAATLCSFGFRFLKAFFLLPER 213

RESULT 7  
 08T8Y5 PRELIMINARY; PRT; 299 AA.  
 ID 08T8Y5;  
 AC 08T8Y5;  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

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DE AT16536P.
GN BUFFY.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

RN
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Abdayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nuno J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY05219; AAL68086.1; -.
SQ SEQUENCE 299 AA; 33379 MW; 7FB125A6B323B23 CRC64;

Query Match 20.8%; Score 183; DB 5; Length 299;
Best Local Similarity 26.9%; Pred. No. 3e-09;
Matches 56; Conservative 26; Mismatches 60; Indels 66; Gaps 8;

OY 25 KETVQAKALGREYVHARLLRAGL-----SWGAP----- 53
DB 87 QDIISGRCGLGCHYIKRRLRSGLNKKLGIORISLSTSMGIYRDVFPVAVYGLDEL 146
OY 54 ERASPA-----PGGR-----LAECYVLLRLGITWGSVLSVAGL 91
DB 147 ERMHRIYNGVARQICRNNGGFEHPDVAISLLGAVGRELFVEITWSVISLFAIAGL 206
OY 92 AVDCVRQAPAVAHVLDLGEFVKRTLATWLRRGW---TDVLKCVSTDPGFRSHW 147
DB 207 SYDCVRQGHPEYLPKLMESEVIEDVLPWINEGMSGINTHVLPTTNSLNP---LEW 263
OY 148 LVATL-CSFG-----RLKAFELLPE 169
DB 264 TTLVIGVVFGLLVFMILRFITNLIVPK 291

RESULT 8
O9NGX3 PRELIMINARY: PRT: 313 AA.
AC O9NGX3:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Bcl-2-like protein BUFFY (Fragment).
OS Drosophila melanogaster (Fruit fly).
GN BUFFY OR CG8238.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

RN
RP SEQUENCE FROM N.A.
RA Colussi P.A., Quinn L.M., Huang D.C., Coombe M., Read S.H.,
RA Richardson H., Kumar S.
DE Bcl-2, a proapoptotic bcl-2 homologue, is a component of the
RT Drosophila melanogaster cell death machinery.
RL J. Cell Biol. 148:703-714(2000).
DR EMBL: AF237864; AAF44120.1; -.
DR HSSP: Q07817; 1MAZ.
DR FLYBase: FBgn0040491; BUffy.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR002475; Bcl2_family.
DR Pfam: PF00452; Bcl-2_1.
DR SMART: SM00337; BCL_1.
DR PROSITE: PS50062; BCL2_FAMILY_1.
FT NON_TER 1
SQ SEQUENCE 313 AA; 34909 MW; 775A41FDD5B678E CRC64;

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Query Match 20.8%; Score 183; DB 5; Length 313;
Best Local Similarity 26.9%; Pred. No. 3.2e-09;
Matches 56; Conservative 26; Mismatches 60; Indels 66; Gaps 8;

OY 25 KETVQAKALGREYVHARLLRAGL-----SWGAP----- 53
DB 101 QDIISGRCGLGCHYIKRRLRSGLNKKLGIORISLSTSMGIYRDVFPVAVYGLDEL 160
OY 54 ERASPA-----PGGR-----LAECYVLLRLGITWGSVLSVAGL 91
DB 161 ERMHRIYNGVARQICRNNGGFEHPDVAISLLGAVGRELFVEITWSVISLFAIAGL 220
OY 92 AVDCVRQAPAVAHVLDLGEFVKRTLATWLRRGW---TDVLKCVSTDPGFRSHW 147
DB 221 SYDCVRQGHPEYLPKLMESEVIEDVLPWINEGMSGINTHVLPTTNSLNP---LEW 277
OY 148 LVATL-CSFG-----RLKAFELLPE 169
DB 278 TTLVIGVVFGLLVFMILRFITNLIVPK 305

RESULT 9
O9V612 PRELIMINARY: PRT: 247 AA.
AC O9V612:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CG8238 protein.
OS Drosophila melanogaster (Fruit fly).
GN BUFFY OR CG8238.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

RN
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132.
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abirl J.F., Abdayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferrara C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jajala M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Koshnell A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon R., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheelers F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaes R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

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RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003825; AAF58628.1; -.  
 DR HSSP: Q07817; 1MA2.  
 DR FlyBase: FBgn0040491; Buffy.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR002475; Bcl2\_family.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PSS0062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 247 AA; 27466 MW; A2C4325FAFC1620 CRC64;  
 Query Match 19.8%; Score 173.5; DB 5; Length 247;  
 Best Local Similarity 27.8%; Pred. No. 1.9e-08;  
 Matches 44; Conservative 20; Mismatches 41; Indels 53; Gaps 4;  
 QY 25 KEIVQAQKALGREYVHARLLRAGL-----SWSNP----- 53  
 DB 87 QDIISGRCLCGHYIKRRLRRSGLFNKKIGLQIRISILGSTSGYRDPFNAVQVLGDEL 146  
 QY 54 ERASPA-----PGR-----LAECYVLLRLGTTGKVSLSYVAAGL 91  
 DB 147 ERMHPRITNGVARQICRNGGEPDPDAVSLLGAVGRELFVEITWSKVISLFAIAGL 206  
 QY 92 AVDCVQAQAPAMVHALVDCIGFEVRKTLATPWLRRRGW 129  
 DB 207 SYDCVQGHPEYLPKLMESYSEVIEDLPVWINGGW 244  
 RESULT 10  
 ID 09V9C8 PRELIMINARY; PRT: 300 AA.  
 AC 09V9C8:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Death EXECUTORER BCL-2 homolog protein (PROAPOPTOTIC BCL-2 homolog  
 DE DEBCL) (BCL-2 family member protein) (BCL-2 ORTHOLOG DBORG-1).  
 GN DEBCL OR DBORG1 OR BOK OR BCL2 OR BCL1 OR ROB-1 OR CG12397.  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; *Drosophila*.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=EMBRYO;  
 RX MEDLINE=20105529; PubMed=2015529;  
 RA Igaki T., Kanuka H., Inohara N., Sawamoto K., Nunez G., Okano H.,  
 RA Miura M.;  
 RT "Drob-1, a *Drosophila* member of the Bcl-2/CED-9 family that promotes  
 RT cell death.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:662-667(2000).  
 RL [2]  
 RP REVISIONS TO N-TERMINUS.  
 RA Igaki T., Kanuka H., Inohara N., Sawamoto K., Okano H., Miura M.;  
 RL Submitted (SEP-1999) to the EMBL/Genbank/DBD databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20153510; PubMed=10684252;  
 RA Colussi P.A., Quinn L.M., Huang D.C.S., Coombe M., Read S.H.,  
 RA Richardson H., Kumar S.;  
 RT "debc1, a proapoptotic Bcl-2 homologue, is a component of the  
 RT *Drosophila melanogaster* cell death machinery.";  
 RL J. Cell Biol. 148:703-714(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Zheng H., Huang Q., Ke N., Matsuyama S., Hammock B., Godzik A.,  
 RA Reed J.C.;  
 RT "Drosophila pro-apoptotic Bcl-2/Bax homolog reveals evolutionary  
 RT conservation of cell death mechanisms.";

RL J. Biol. Chem. 0:0-0(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,  
 RA Abilil J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,  
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferlita S., Fleischmann W.,  
 RA Fostel C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Modarri C., Morris J., Mostrel A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Kurada P., White K.;  
 RT "Putative *Drosophila* homolog of mammalian Bcl-2-related ovarian killer  
 RT protein.";  
 RN Submitted (DEC-1999) to the EMBL/Genbank/DBD databases.  
 RL [7]  
 RP SEQUENCE FROM N.A.  
 RA Zhou L., Steller H.;  
 RT "Potential *Drosophila* homologue of Bcl-2-related ovarian killer  
 RT (BOK)."  
 RL Submitted (JAN-2000) to the EMBL/Genbank/DBD databases.  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RA Brachmann C.B., Jassim O.W., Wachsmuth B.D., Cagan R.L.;  
 RT "dborg-1, a *Drosophila* Bcl-2 family member that functions in the  
 RT apoptotic response to UV-irradiation.";  
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBD databases.  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RX EMBL: AB032430; BAA89603.2; -.  
 DR EMBL: AF149798; AAF26841.1; ALT\_INT.  
 DR EMBL: AF178430; AAF26289.1; -.  
 DR EMBL: AF228044; AAF69165.1; -.  
 DR EMBL: AE003789; AAF57365.1; ALT\_TERM.  
 DR EMBL: AF216752; AAF25955.1; ALT\_TERM.  
 DR EMBL: AF222004; AAF44324.1; -.  
 DR EMBL: AF244352; AAF44714.1; -.  
 DR FlyBase: FBgn0029131; debcl.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR002475; Bcl2\_family.  
 DR InterPro: IPR000822; Znf\_C2H2.

DR Pfam: PF00452; Bcl-2; 1.  
DR SMART: SM00337; BCL1.  
DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
DR PROSITE: PS50157; ZINC\_FINGER\_C2H2\_2; 4.  
KW DNA-binding; zinc-finger.  
FT CONFLICT 1 86 MISSING (IN REF. 4).  
FT CONFLICT 215 215 I->V (IN REF. 1).  
FT CONFLICT 217 217 C->R (IN REF. 4).  
GN CONFLICT 217 217  
SO SEQUENCE 300 AA; 32940 MW; FF29E0ADCDF3D0942 CRC64;

Query Match 19.7%; Score 173; DB 5; Length 300;  
Best Local Similarity 28.2%; Pred. No. 2.6e-08;  
Matches 44; Conservative 17; Mismatches 43; Indels 52; Gaps 3;

OY 26 ELVNAQAKLGRYVHARLRAG-LSMSAPER----- 55  
DB 96 DIINGKCLCGYIRARRAGVLRNRYQRLNILDPGSSHVYVEVPALNSMGEELER 155  
OY 56 -----ASPAPGRLAE-----VCTVLLRLGITWGKVSLYSVAAGLAV 93  
DB 156 MHPRYTINISROLSPRPFGELESDMAPMLNLVAKDLFRSSITWGIITIFAVCGGFAT 215  
OY 94 DCVROAPAMVHALVDCIGEFVVRK--TLATWLRRRGG 129  
DB 216 DCVROGHFDYQLCLIDGLAEITIEDLVYWLIDNGM 251

## RESULT 11

O95083 PRELIMINARY; PRT; 317 AA.

ID O95083  
AC O95083  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE GH01265P.  
GN DEBCL OR CG12397.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BERKELEY;  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
RA Gonzalez M., Guartin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;  
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AY058249; AAL13478.1; -.  
DR FlyBase: FBgn0029131; debcl.  
DR InterPro: IPR000712; BCL2\_BH.  
DR Pfam: PF00452; Bcl-2; 1.  
DR SMART: SM00337; BCL1.  
SO SEQUENCE 317 AA; 34649 MW; 46B22FEDICCG6F01F CRC64;

Query Match 16.2%; Score 142; DB 5; Length 317;  
Best Local Similarity 27.4%; Pred. No. 2.2e-05;  
Matches 43; Conservative 18; Mismatches 42; Indels 54; Gaps 4;

OY 26 ELVNAQAKLGRYVHARLRAG-LSMSAPER----- 55  
DB 96 DIINGKCLCGYIRARRAGVLRNRYQRLNILDPGSSHVYVEVPALNSMGEELER 155  
OY 56 -----ASPAPGRLAE-----VCTVLLRLGITWGKVSLYSVAAGLAV 93  
DB 156 MHPRYTINISROLSPRPFGELESDMAPMLNLVAKDLFRSSITWGIITIFAVCGGFAT 215  
OY 94 DCVROAPAMVHALVDCIGEFVVRK--TLATWLRRRGG 129  
DB 216 DCVROGHFDYQLCLIDGLAEITIEDLVYWLIDNGM 252

RESULT 12  
O923R6  
ID O923R6 PRELIMINARY; PRT; 236 AA.  
AC O923R6  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE B-cell lymphoma protein 2.  
GN BCL2.  
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Cricetus.  
OX NCBI\_TaxID=10030;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Lai D.Z., Chen W., Wang H.T.;  
RT "Construction of a robust CHO cell line for biopharmaceutical use."  
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF404339; AAK92201.1; -.  
DR InterPro: IPR000712; BCL2\_BH.  
DR InterPro: IPR003093; BCL2\_BH4.  
DR InterPro: IPR002475; BCL2\_family.  
DR InterPro: IPR004725; BCL2\_reg.  
DR Pfam: PF00452; Bcl-2; 1.  
DR Pfam: PF02180; BH4; 1.  
DR TIGRFAMs: TIGR00865; bcl-2; 1.  
DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
DR PROSITE: PS01080; BH1; UNKNOWN.1.  
DR PROSITE: PS01258; BH2; UNKNOWN.1.  
DR PROSITE: PS01259; BH3; UNKNOWN.1.  
DR PROSITE: PS01260; BH4\_1; UNKNOWN.1.  
DR PROSITE: PS50063; BH4\_2; 1.  
SO SEQUENCE 236 AA; 26500 MW; BEDF052EF32CA8B8 CRC64;

Query Match 14.4%; Score 126.5; DB 11; Length 236;  
Best Local Similarity 18.9%; Pred. No. 0.00045;  
Matches 40; Conservative 25; Mismatches 36; Indels 91; Gaps 4;

OY 28 VAQAKALG-----REYVHARLRAGLSW-----SAPERASAPAG----- 61  
DB 1 MAQAGRTGYDNEIYMKYIHYKLSQGYEMDGVDAAPLGAAPPGJFSPQESNPPIA 60  
OY 62 ----- 61  
DB 61 VHRDMAARTPLRPVATGTPTLSPVPVHILTRRAGDDFSRRYRDPFAEMSSQLHTLP 120  
OY 62 -----GLAEVCVLLRLGITWGKVSLYSVAAGLAVDCVROAPAMVHALVDCIGEFVVRK 117  
DB 121 FTARGRFATVVEELFRDGVNMGRIYAFEPFGVCMCVESVNRMSPLVDNIALMTEYLNR 180  
OY 118 TLATWLRRRGGWTDVLCV-VSTDGPFRRSHWL 148  
DB 181 HHTWIDNGMGDAFVELYGPVRLPDPFSLW 212

RESULT 13  
O919N4  
ID O919N4 PRELIMINARY; PRT; 192 AA.  
AC O919N4  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Bax.  
GN BAX.  
OS Brachydanio rerio (zebrafish) (zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.

```

RX MEDLINE-20373792; PubMed-10917738;
RA Inohara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
   zebrafish."
RL Cell Death Differ. 7:509-510(2000).
DR EMBL; AF231015; AAF66960.1; -.
DR HSSP; P53563; IAF3.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL.1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
SQ SEQUENCE 192 AA; 21401 MW; 8A71A630A56FDC32 CRC64;

Query Match 12.5%; Score 109.5; DB 13; Length 192;
Best Local Similarity 21.0%; Pred. No. 0.014; Indels 35; Gaps 4;
Matches 34; Conservative 29; Mismatches 64;

OY 6 NSSVFAEIMDAFDRSPDKELVAQAKALGREYVHARLLAQLSWAPERASPARGRLA 65
DB 45 RSQLGVEICD-----PSHKRLAQCLQIGDELQDGNALQSLMN-----NSNIQ 88
OY 66 EVCYVLLRLG-----ITWGVSLYSVAAGLAVDCVROAPAMVHALVDCIGEFVRK 117
DB 89 PTQDFIRVAREIFSDGKFMGRVVALFEACRLVKAISTRVPIIRTIIISWTMSYIOE 148
OY 118 TLATVLRRCGWTDLVKCVSTDPGFRSHMLVATLCSFGRL 159
DB 149 HYINMIREGGW-----DGIRSFYGTPTQGTQVFL 179

RESULT 14
OY9N36 PRELIMINARY; PRT; 219 AA.
AC O9N36;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE B-cell leukemia/lymphoma x-gamma (Fragment).
GN BCLX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Yang X.-F., Cantor H.;
RT "Novel cDNA structure and genomic organization of apoptosis regulatory
   gene Bcl-x-gamma."
RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF133279; AAK15454.1; -.
DR EMBL; AF133281; AAK15454.1; JOINED.
DR HSSP; P53563; IAF3.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL.1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01259; BH3; 1.
FT NON_TER 1
SQ SEQUENCE 219 AA; 24224 MW; EB352ECACFAA6AF5 CRC64;

Query Match 12.5%; Score 109.5; DB 11; Length 219;
Best Local Similarity 25.0%; Pred. No. 0.016; Indels 15; Gaps 3;
Matches 25; Conservative 17; Mismatches 43;

OY 66 EVCYVLLRLGITWGVSLYSVAAGLAVDCVROAPAMVHALVDCIGEFVRKTLATWLR 125
DB 109 QVNNELFRDGVNMGRIVAFESFGALCVESVDKEMQVLSRIASMMATYLDNLHPWIOE 168
OY 126 RCGW-----TDVLKCVSTDPGFRSH-----WLVAT 151

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DB 169 NGMGVSGGCTPLRSVFRRLVQV-PGVAEHVCDPSLWEVET 207
RESULT 15
AC O35843 PRELIMINARY; PRT; 235 AA.
ID O35843;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Bcl-x-gamma.
GN BCL2L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6/CBA; TISSUE=THYMUS;
RX MEDLINE-98051053; PubMed-9390687;
RA Yang X.-F., Weber G.F., Cantor H.;
RT "A novel Bcl-x isoform connected to the T cell receptor regulates
   apoptosis in T cells."
RL Immunity 7:629-639(1997).
DR EMBL; U51277; AAC53458.1; -.
DR HSSP; P53563; IAF3.
DR MGI; MGI:88139; Bcl2L.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL.1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 235 AA; 26122 MW; 649D914C2D5378F6 CRC64;

Query Match 12.5%; Score 109.5; DB 11; Length 235;
Best Local Similarity 25.0%; Pred. No. 0.017; Indels 15; Gaps 3;
Matches 25; Conservative 17; Mismatches 43;

OY 66 EVCYVLLRLGITWGVSLYSVAAGLAVDCVROAPAMVHALVDCIGEFVRKTLATWLR 125
DB 125 QVNNELFRDGVNMGRIVAFESFGALCVESVDKEMQVLSRIASMMATYLDNLHPWIOE 184
OY 126 RCGW-----TDVLKCVSTDPGFRSH-----WLVAT 151
DB 185 NGMGVSGGCTPLRSVFRRLVQV-PGVAEHVCDPSLWEVET 223

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Search completed: April 29, 2003, 11:25:40  
 Job time : 22.7493 secs



GenCore version 5.1.4p5\_4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:18:26 ; Search time 5.99217 Seconds

(without alignments)  
1176.699 Million cell updates/sec

Title: US-09-682-667-4

Perfect score: 878

Sequence: 1 MEVLRRSSVFPAEIMDAFDR.....TLCSFGRLKAFILLPER 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	137	15.6	236	1 BCL2_RAT	P49950 ratu
2	130	14.8	239	1 BCL2_HUMAN	P10415 homo sapien
3	129	14.7	229	1 BCL2_BOVIN	002718 bos taurus
4	128	14.6	236	1 BCL2_CRITO	091417 mus musculus
5	127	14.5	236	1 BCL2_MOUSE	000709 gallus galli
6	113	12.9	233	1 BCL2_CHICK	091827 xenopus lae
7	110	12.5	228	1 ARL_XENLA	P53563 ratu
8	107	12.2	233	1 BCLX_RAT	007816 gallus galli
9	105.5	12.0	229	1 BCLX_CHICK	064373 sus scrofa
10	105	12.0	233	1 BCLX_MOUSE	077737 sus scrofa
11	104	11.8	233	1 BCLX_PIG	007817 homo sapien
12	103	11.7	233	1 BCLX_HUMAN	007814 homo sapien
13	101	11.5	218	1 BAXB_HUMAN	P70345 mus musculus
14	100	11.4	193	1 BCLM_MOUSE	091828 xenopus lae
15	99	11.3	204	1 ARL1_XENLA	Q16611 homo sapien
16	97	11.0	211	1 BAK_HUMAN	007812 homo sapien
17	96	10.9	193	1 BAXA_HUMAN	092842 homo sapien
18	96	10.9	192	1 BCLM_HUMAN	007813 mus musculus
19	95	10.8	192	1 BAXA_MOUSE	063590 ratu
20	95	10.8	192	1 BAXA_MOUSE	007813 mus musculus
21	94	10.7	208	1 BAK_MOUSE	007813 mus musculus
22	93.5	10.6	143	1 BAXD_HUMAN	002703 bos taurus
23	93	10.6	192	1 BAXA_BOVIN	013014 homo sapien
24	87	9.9	211	1 BAK2_HUMAN	007440 mus musculus
25	83.5	9.5	172	1 BFL1_MOUSE	P51449 homo sapien
26	80	9.1	535	1 SSOH_MOUSE	P57689 mycobacteri
27	80	9.1	1115	1 CARB_MYCTU	P36641 pseudomonas
28	79	9.0	401	1 PILC_PSEPU	Q16548 homo sapien
29	78	8.9	175	1 BFL1_HUMAN	015274 homo sapien
30	76.5	8.7	297	1 NADC_HUMAN	P45535 mycobacteri
31	75.5	8.6	610	1 RHO_MYCLE	P70289 mus musculus
32	75.5	8.6	1705	1 PTPD_MOUSE	Q9WE14 mus musculus
33	75	8.5	1300	1 IRR_MOUSE	

34	74.5	8.5	602	1 RHO_MYCTU	Q10607 mycobacteri
35	74.5	8.5	728	1 VIV_ORYSA	P37398 oryza sativ
36	73.5	8.4	350	1 MCIL_HUMAN	007820 homo sapien
37	73	8.3	378	1 MYI2_MYCTU	Q10400 mycobacteri
38	72.5	8.3	177	1 NR13_COTJA	Q90343 coturnix co
39	72.5	8.3	539	1 TCPZ_CAEL	P46550 caenorhabdi
40	72.5	8.3	1597	1 DVAL_DICVI	Q24702 dicycosculu
41	72	8.2	370	1 IDI2_PYRAB	Q94259 pyrococcus
42	72	8.2	517	1 CRT1_MYXXA	P54879 myxococcus
43	71.5	8.1	438	1 Y485_MYCTU	Q11151 mycobacteri
44	71.5	8.1	1121	1 CARB_MYCLE	Q9C82 mycobacteri
45	71	8.1	288	1 FIXA_BRAVA	P53577 bradyrhizob

## ALIGNMENTS

RESULT 1	ID	Accession	Standard	PRT	236 AA.
BCL2_RAT	AC	P49950	062837	064032	
BCL2_RAT	AC	P49950	062837	064032	
01-OCT-1996 (Rel. 34, Created)	DT	01-OCT-1996 (Rel. 34, Created)			
01-NOV-1997 (Rel. 35, Last sequence update)	DT	01-NOV-1997 (Rel. 35, Last sequence update)			
15-JUN-2002 (Rel. 41, Last annotation update)	DT	15-JUN-2002 (Rel. 41, Last annotation update)			
Apoptosis regulator Bcl-2.	DE	Apoptosis regulator Bcl-2.			
BCL2 OR BCL-2.	DE	BCL2 OR BCL-2.			
Rattus norvegicus (Rat).	OS	Rattus norvegicus (Rat).			
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
NCBI_Taxid=10116;	OX	NCBI_Taxid=10116;			
(1)	RP	(1)			
SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.			
TISSUE=Brain;	RC	TISSUE=Brain;			
MEDLINE=94193015; PubMed=8144041;	RX	MEDLINE=94193015; PubMed=8144041;			
Sato T., Irie S., Kravetski S., Reed J.C.;	RA	Sato T., Irie S., Kravetski S., Reed J.C.;			
"Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";	RT	"Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";			
Gene 140:291-292(1994).	RL	Gene 140:291-292(1994).			
(2)	RP	(2)			
SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.			
STRAIN=Sprague-Dawley; TISSUE=Ovary;	RC	STRAIN=Sprague-Dawley; TISSUE=Ovary;			
MEDLINE=95129487; PubMed=7828536;	RX	MEDLINE=95129487; PubMed=7828536;			
Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;	RA	Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;			
"Expression of members of the bcl-2 gene family in the immature rat	RT	"Expression of members of the bcl-2 gene family in the immature rat			
ovary: equine chorionic gonadotropin-mediated inhibition of granulosa	RT	ovary: equine chorionic gonadotropin-mediated inhibition of granulosa			
cell apoptosis is associated with decreased bax and constitutive	RT	cell apoptosis is associated with decreased bax and constitutive			
bcl-2 and bcl-xlong messenger ribonucleic acid levels.";	RT	bcl-2 and bcl-xlong messenger ribonucleic acid levels.";			
Endocrinology 136:232-241(1995).	RL	Endocrinology 136:232-241(1995).			
(3)	RP	(3)			
SEQUENCE OF 19-172 FROM N.A.	RP	SEQUENCE OF 19-172 FROM N.A.			
MEDLINE=95059917; PubMed=7969891;	RX	MEDLINE=95059917; PubMed=7969891;			
Castren E., Ohga Y., Bertzagh M.P., Tsimogiorgis G., Thoenen H.,	RA	Castren E., Ohga Y., Bertzagh M.P., Tsimogiorgis G., Thoenen H.,			
Lindholm D.;	RT	Lindholm D.;			
"bcl-2 messenger RNA is localized in neurons of the developing and	RT	"bcl-2 messenger RNA is localized in neurons of the developing and			
adult rat brain.";	RT	adult rat brain.";			
Neuroscience 61:165-177(1994).	RL	Neuroscience 61:165-177(1994).			
-I- FUNCTION: Suppresses apoptosis in a variety of cell systems	CC	-I- FUNCTION: Suppresses apoptosis in a variety of cell systems			
including factor-dependent lymphohematopoietic and neural cells.	CC	including factor-dependent lymphohematopoietic and neural cells.			
Regulates cell death by controlling the mitochondrial membrane	CC	Regulates cell death by controlling the mitochondrial membrane			
permeability. Appears to function in a feedback loop system with	CC	permeability. Appears to function in a feedback loop system with			
caspases. Inhibits caspase activity either by preventing the	CC	caspases. Inhibits caspase activity either by preventing the			
release of cytochrome c from the mitochondria and/or by binding to	CC	release of cytochrome c from the mitochondria and/or by binding to			
the apoptosis-activating factor (APAF-1).	CC	the apoptosis-activating factor (APAF-1).			
-I- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAK and	CC	-I- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAK and			
Bcl-x(L). Heterodimerization with BAX requires intact BHL and BH2	CC	Bcl-x(L). Heterodimerization with BAX requires intact BHL and BH2			
domains, and is necessary for anti-apoptotic activity (By	CC	domains, and is necessary for anti-apoptotic activity (By			
similarity). Also interacts with APAF-1 and RA-1 (By similarity).	CC	similarity). Also interacts with APAF-1 and RA-1 (By similarity).			
-I- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular	CC	-I- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular			
membrane of the nuclear envelope and the endoplasmic reticulum.	CC	membrane of the nuclear envelope and the endoplasmic reticulum.			
-I- TISSUE SPECIFICITY: Expressed in a variety of tissues, with	CC	-I- TISSUE SPECIFICITY: Expressed in a variety of tissues, with			
highest levels in reproductive tissues. In the adult brain,	CC	highest levels in reproductive tissues. In the adult brain,			
expression is localized in mitral cells of the olfactory bulb,	CC	expression is localized in mitral cells of the olfactory bulb,			
granule and pyramidal neurons of hippocampus, ponting nuclei,	CC	granule and pyramidal neurons of hippocampus, ponting nuclei,			
cerebellar granule neurons, and in ependymal cells. In prenatal	CC	cerebellar granule neurons, and in ependymal cells. In prenatal			

brain, expression is higher and localized in the neuroepithelium and in the cortical plate.  
- DOMAIN: The Bcl-2 domain is required for anti-apoptotic activity and for interaction with Raf-1 (By similarity).  
- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl-2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl-2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.  
- PTM: Phosphorylated by protein phosphatase 2A (PP2A) (By similarity).  
- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the Bcl-2 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).  
- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BHL1) DOMAIN.  
- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BHL2) DOMAIN.  
- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BHL3) DOMAIN.  
- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BHL4) DOMAIN.  
- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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DR EMBL: L14680; AAA53662.1; -  
DR EMBL: U34964; AAA77687.1; -  
DR EMBL: S74122; -; NOT\_ANNOTATED\_CDS.  
DR HSSP: Q07817; 1MAZ.  
DR InterPro: IPR002475; BCL2\_family.  
DR InterPro: IPR000712; Bcl2\_BH.  
DR InterPro: IPR003093; Bcl2\_BH.  
DR InterPro: IPR004725; Bcl2\_reg.  
DR Pfam: PF00452; Bcl-2; 1.  
DR Pfam: PF02180; BH4; 1.  
DR SMART: SM00337; BCL; 1.  
DR SMART: SM00265; BH4; 1.  
DR TIGRFAMs: TIGR00865; bcl-2; 1.  
DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
DR PROSITE: PS01080; BH1; 1.  
DR PROSITE: PS01258; BH2; 1.  
DR PROSITE: PS01259; BH3; 1.  
DR PROSITE: PS01260; BH4\_1; 1.  
DR PROSITE: PS50063; BH4\_2; 1.  
KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
FT DOMAIN 10 30 BH4.  
FT DOMAIN 90 104 BH3.  
FT DOMAIN 133 152 BH1.  
FT DOMAIN 184 199 BH2.  
FT TRANSMEM 209 230 POTENTIAL.  
FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
FT MOD\_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
FT CONFLICT 42 42 A -> R (IN REF. 2).  
FT CONFLICT 157 157 E -> G (IN REF. 1).  
FT CONFLICT 164 164 S -> Y (IN REF. 2).  
FT CONFLICT 212 212 L -> Q (IN REF. 2).  
SQ SEQUENCE 236 AA; 26622 MW; E7688CB9071A872A CRC64;

Query Match 15.6%; Score 137; DB 1; Length 236;  
Best Local Similarity 20.5%; Pred. No. 2.6e-06;  
Matches 45; Conservative 25; Mismatches 57; Indels 92; Gaps 5;

QY 28 VQAQALG-----REYVHARLLRAGLSW-----SAPERASPPAG----- 61  
DB 1 MAQAGRTGYDNRREIYMKIYHKLRSQRYEMWDGDEDSAPLRAAPFGIFSPESNRTPA 60  
QY 62 ----- 61  
DB 61 VHRDTAARTSPLRPLVANAGPALSPVPVYHLTLRRAGDDFSRRYRDRFAEKSSQLHLTP 120

QY 62 ----GRLAECVTYLLRLGITMGKVVSLYSVAAGLAVDCYRQAPMVAHVLCIGFEVRK 117  
DB 121 FARGSGFAIVVELPRDGYNMGRIVAFEEFGVMCVESNRRMSPLYVDIAIMNEYLR 180  
QY 118 TLATWLRRRGGWTDVLCV-VSTDEGFNRSHWL-VATLCS 134  
DB 181 HLHTWIDNGWDVAVEYLGPSMRPLDFRSWLSLTLIS 219

RESULT 2  
BCL2\_HUMAN  
ID BCL2\_HUMAN STANDARD; PRT; 239 AA.  
AC P10415; P10416; Q16197; Q13842;  
DT 01-MAR-1989 (Rel. 10, Created)  
DR 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptosis regulator Bcl-2.  
GN BCL2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).  
RX MEDLINE=86259760; PubMed=3523487;  
RA Tsujimoto Y., Croce C.M.;  
RT "Analysis of the structure, transcripts, and protein products of bcl-2, the gene involved in human follicular lymphoma.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).  
RN [2]  
RP REVISIONS TO 96; 110 AND 237.  
RX MEDLINE=92375724; PubMed=1508712;  
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;  
RT "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";  
RL Nucleic Acids Res. 20:4187-4192(1992).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
RX MEDLINE=87002488; PubMed=2875799;  
RA Cleary M.L., Smith S.D., Sklar J.;  
RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin transcript resulting from the t(14;18) translocation.";  
RL Cell 47:19-28(1986).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
RX MEDLINE=88196071; PubMed=2834197;  
RA Seto M., Jaeger U., Hockett R.D., Gruninger W., Bennett S., Goldman P., Korsmeyer S.J.;  
RT "Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2-Ig fusion gene in lymphoma.";  
RL EMBO J. 7:123-131(1988).  
RN [5]  
RP SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS NHL.  
RX MEDLINE=92096610; PubMed=1339299;  
RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.;  
RT "Frequent incidence of somatic mutations in translocated BCL2 oncogenes of non-Hodgkin's lymphomas.";  
RL Blood 79:229-237(1992).  
RN [6]  
RP SUBCELLULAR LOCATION.  
RX MEDLINE=91066924; PubMed=2250705;  
RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.;  
RT "Bcl-2 is an inner mitochondrial membrane protein that blocks programmed cell death.";  
RL Nature 348:334-336(1990).  
RN [7]  
RP MUTAGENESIS.  
RX MEDLINE=94239528; PubMed=8183370;  
RA Yin X.-M., Oltvai Z.N., Korsmeyer S.J.;  
RT "BH1 and BH2 domains of Bcl-2 are required for inhibition of

RT apoptosis and heterodimerization with Bax.";  
 RL Nature 369:321-323(1994).  
 RN [8]  
 RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.  
 RX MEDLINE-98057466; PubMed-9395403;  
 RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,  
 RA Ueno K., Hardwick J.M.;  
 RT "Conversion of Bcl-2 to a Bax-like death effector by caspases.";  
 RL Science 278:1966-1988(1997).  
 RN [9]  
 RP REVIEW ON PHOSPHORYLATION.  
 RX MEDLINE-21260650; PubMed-11368354;  
 RA Ruvolo P.P., Deng X., May W.S.;  
 RT "Phosphorylation of Bcl2 and regulation of apoptosis.";  
 RL Leukemia 15:515-522(2001).  
 RN [10]  
 RP PHOSPHORYLATION BY ASK1/JNK1.  
 RX MEDLINE-20036804; PubMed-10567572;  
 RA Yamamoto K., Ichijo H., Korsmeyer S.J.;  
 RT "Bcl-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal  
 RT protein kinase pathway normally activated at G(2)/M.";  
 RL Mol. Cell. Biol. 19:8469-8478(1999).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (Apaf-1).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(l). Heterodimerization with BAX requires intact BH1 and BH2  
 CC domains, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with Apaf-1 and RAf-1.  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;  
 CC are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 CC for interaction with RAf-1.  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle. In the absence of  
 CC growth factors, Bcl2 appears to be phosphorylated by other protein  
 CC kinases such as ERKs and stress-activated kinases.  
 CC -1- DEPHOSPHORYLATED BY protein phosphatase 2A (PP2A) (By similarity).  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity.  
 CC -1- DISEASE: Involved in follicular lymphoma (FL) (also known as type  
 CC II chronic lymphatic leukemia) by a chromosomal translocation  
 CC t(14;18)(q32;q21) which involves Bcl2 and immunoglobulin gene  
 CC regions.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;  
 CC WWW-http://www.infobiogen.fr/services/chronocancer/Genes/BCL2ID49.html".  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL: M13994; AAA51813.1; ALT-SEQ.  
 DR EMBL: M13995; AAA51814.1; ALT-SEQ.

DR EMBL: M14745; AAA55591.1; -;  
 DR EMBL: X06487; CAA29778.1; -;  
 DR EMBL: S72602; AAD14111.1; ALT-SEQ.  
 DR PIR: A29409; TVH0A1.  
 DR PIR: B29409; TVH0B1.  
 DR PIR: A24428; TVH0BC.  
 DR PIR: C37332; C37332.  
 DR PIR: D37332; D37332.  
 DR HSSP: O07817; 1MAZ.  
 DR Genew: HGNC:990; BCL2.  
 DR MIM: 151430; -;  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 KW Proto-oncogene; Apoptosis; Bcl-2; 1.  
 KW Mitochondrion; Phosphorylation; Alternative splicing; Transmembrane;  
 KW Chromosomal translocation;  
 KW Polymorphism; Disease mutation.  
 KW DOMAIN 10 30  
 FT DOMAIN 93 107  
 FT DOMAIN 136 155  
 FT DOMAIN 187 202  
 FT TRANSMEM 212 233  
 FT SITE 34 35  
 FT MOD\_RES 70 70  
 FT VARSPIC 196 239  
 FT VARIANT 7 7  
 FT VARIANT 59 59  
 FT VARIANT 93 93  
 FT VARIANT 145 145  
 FT MUTAGEN 34 34  
 FT MUTAGEN 64 64  
 FT MUTAGEN 145 145  
 FT MUTAGEN 188 188  
 FT CONFLICT 48 48  
 FT CONFLICT 59 59  
 FT CONFLICT 117 117  
 FT CONFLICT 129 129  
 SQ SEQUENCE 239 AA; 26266 MW; 3C49F2B714DC9CB CRC64;  
 Query Match 14.8%; Score 130; DB 1; Length 239;  
 Best Local Similarity 19.4%; Pred. No. 1; 3e-05;  
 Matches 40; Conservative 25; Mismatches 53; Indels 88; Gaps 4;  
 QY 37 EYVHARLLRAGLSM-----SAPERASPARC----- 61  
 DB 17 KYIHYSKSGYEMDADGVAAPGAPACITSSQPGHPRHRAASDPARTSPLOTPTA 76  
 QY 62 -----GRLAEYCTV 70  
 DB 77 APCAAGPALSPVPVYHLTLRQAGDEFSRRYRRDFAEMSSQLHLPTFARGFATVVEE 136  
 QY 71 LFLGLITWGVSLYSVAGLAVDCYRQAPAAVYHALVCLGFFVKTLATWLRRGGW 130  
 DB 137 LFRDGVNCRIVAFPEFGVGVESVNRKMSPLVDNIALIMWTEYLNRHLTLTWIDNGMD 196

QY 131 DVLKCV-VSTDPEFSHWL-VATLCS 154  
 DB 197 AFVELYGPMSRPLDFPSWLSLTKLLS 222

RESULT 3  
 BCL2\_BOVIN STANDARD: PRT: 229 AA.

AC 002718;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBT\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Holstein; TISSUE=Thymus;  
 RA Reyes R.A., Cockrell G.L.;  
 RT "Bovine leukemia virus associated leukemogenesis is correlated with suppression of programmed cell death and increased expression of Bcl-2."  
 RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RL -1- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1) (By similarity).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum (By similarity).  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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 CC EMBL: U92434; AAB53319.1; -  
 DR HSSP: 007817; IMAZ  
 DR InterPro: IPR002475; BCL2\_family.

DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
 FT DOMAIN 10 30  
 FT DOMAIN 64 68 POLY-PRO.  
 FT DOMAIN 69 72 POLY-ALA.  
 FT DOMAIN 83 97 BH3.  
 FT DOMAIN 126 145 BH1.  
 FT DOMAIN 177 192 BH2.  
 FT TRANSMEM 202 223 POTENTIAL.  
 FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
 FT MOD\_RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
 SQ SEQUENCE 229 AA: 25099 MW: ADIDDOAF98FFP1ID CRC64;

Query Match 14.7%; Score 129; DB 1; Length 229;  
 Best Local Similarity 19.7%; Pred. No. 1.5e-05;  
 Matches 41; Conservative 25; Mismatches 56; Indels 86; Gaps 4;

QY 37 EYVHALLACLSW-----SAPERASAPG-----GRLAECTVLLRLGITWCK 61  
 DB 17 KTHVHLSRGYEDWAGDAGAAPGAPAGILSSOPGRTAPASRTSPPPPAAGAPAP 76  
 QY 62 -----GLAEVCTVLLRLGITWCK 80  
 DB 77 SPVPVHLLTQAGDDFSRRYRDRFAEMSQLHLPTARERFATVVEELFRDGVNMG 136  
 QY 81 VSLYSVANGADVCRQAPAMVHALVDCLEFVAKTLATLRRRGGTIVLKCV-VST 139  
 DB 137 IVAFFEGGVCMVESYRNREMSPLVDISALMTEYLNRHLHTWIDNGDAVEELGSPSM 196

QY 140 DPGFRSHWLVAATLCSGRFLKAAPELL 167  
 DB 197 RPLDFPSWL-----SLKALLSLAL 215

RESULT 4  
 BCL2\_CRITLO STANDARD: PRT: 236 AA.

AC 09JUV8;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2.  
 OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetulus.  
 OX NCBT\_TaxID=10030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=20431763; PubMed=10973819;  
 RA Tomicic M.T., Christmann M., Kaina B.;  
 RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein."  
 RL Biochem. Biophys. Res. Commun. 275:899-903(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES.  
 RX MEDLINE=21092839; PubMed=11181062;  
 RA Tomicic M.T., Kaina B.;



```

RT      "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9
RT      and caspase-3."
CC      RT      Biochem. Biophys. Res. Commun. 281:404-408(2001).
CC      -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC      including factor-dependent lymphohematopoietic and neural cells.
CC      Regulates cell death by controlling the mitochondrial membrane
CC      permeability. Appears to function in a feedback loop system with
CC      caspases. Inhibits caspase activity either by preventing the
CC      release of cytochrome c from the mitochondria and/or by binding to
CC      the apoptosis-activating factor (APAF-1) (By similarity).
CC      -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC      Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC      domains, and is necessary for anti-apoptotic activity (By
CC      similarity). Also interacts with APAF-1 and RAf-1 (By similarity).
CC      -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC      membrane of the nuclear envelope and the endoplasmic reticulum.
CC      -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC      for interaction with RAf-1 (By similarity).
CC      -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC      anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC      on Ser-70 by PKC is required for the cell cycle (By similarity). In
CC      occurs during the G2/M phase of the cell cycle (By similarity). In
CC      the absence of growth factors, Bcl2 appears to be phosphorylated
CC      by other protein kinases such as ERKs and stress-activated kinases
CC      (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A)
CC      (By similarity).
CC      -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC      cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC      activity, causes the release of cytochrome c into the cytosol
CC      promoting further caspase activity.
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC      -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC      CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      CC      EMBL: AJ271720; CAB92245.1; -.
CC      DR      HSSP: Q07817; IMAZ.
CC      DR      InterPro: IPR002475; BCL2_family.
CC      DR      InterPro: IPR000712; BCL2_BH.
CC      DR      InterPro: IPR003093; BCL2_BH4.
CC      DR      InterPro: IPR004725; BCL2_reg.
CC      DR      Pfam: PF00452; Bcl-2; 1.
CC      DR      Pfam: PF02180; BCL; 1.
CC      DR      SMART: SM00337; BCL; 1.
CC      DR      SMART: SM00265; BH4; 1.
CC      DR      TIGRPFAM: TIGR00865; bcl-2; 1.
CC      DR      PROSITE: PS50062; BCL2_FAMILY; 1.
CC      DR      PROSITE: PS01080; BH1; 1.
CC      DR      PROSITE: PS01258; BH2; 1.
CC      DR      PROSITE: PS01259; BH3; 1.
CC      DR      PROSITE: PS01260; BH4_1; 1.
CC      DR      PROSITE: PS50063; BH4_2; 1.
CC      DR      PROSITE: PS50063; BH4_2; 1.
CC      KW      Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
CC      FT      DOMAIN 10 30 BH4.
CC      FT      DOMAIN 90 104 BH3.
CC      FT      DOMAIN 133 152 BH1.
CC      FT      DOMAIN 184 199 BH2.
CC      FT      TRANSMEM 209 230 BH2.
CC      FT      SITE 64 65 CLEAVAGE (BY CASPASE-3 AND CASPASE-9).
CC      FT      MOD_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
CC      SQ      SEQUENCE 236 AA; 26491 MW; BECADFIEF3337228 CRC64;
Query Match 14.6%; Score 128; DB 1; Length 236;
Best Local Similarity 19.6%; Pred. No. 1.9e-05;

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Matches 43; Conservative 26; Mismatches 58; Indels 92; Gaps 5;
QY      28 VAAKALG-----REYVHARILRAGLSW-----SAPERASAPG----- 61
DB      1 MAQGRGTGYNDREIWMYIHKLSQKGYEMDVGVDYADAPAGAAFTPGIFSPESNPTPA 60
QY      62 ----- 61
DB      61 VHRMARSPRLPRIVATGTGPTLSPPVPVHLTLRRAGDDFSRRYRRDPFAMSQHLTLP 120
QY      62 ----GRAEVCYVLLRLGITWGWKVSLSVAAGLAVDCRQADPAMVHALVDCIGFVRK 117
DB      121 FTARGFRATVVEELFRGVWNGRIYVAFEEFGVGVCSVREMSPLVDNIALMTETYLNR 180
QY      118 TLATVLRGGMTVLCVY-VSTDGPRSHML-VATICS 154
DB      181 HLHTWIDNGMDAFELVYGPVSAPLPDFSWLSKLTLIS 219
RESULT 5
BCL2_MOUSE STANDARD; PRT; 236 AA.
ID      BCL2_MOUSE
AC      P10417; P10418;
DT      01-MAR-1989 (Rel. 10, Created)
DT      01-APR-1993 (Rel. 25, Last sequence update)
DE      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Apoptosis regulator Bcl-2.
GN      BCL2 OR BCL-2.
OS      Mus musculus (mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP      SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC      SPRAIN-BALB/C; TISUP-Liver.
RX      MEDLINE=87187643; PubMed=303245;
RA      Negri M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.;
RT      "Molecular analysis of mcl-2: structure and expression of the murine
RL      gene homologous to the human gene involved in follicular lymphoma.";
RN      Cell 49:455-463(1987).
[2]
RP      REVISIONS TO 221-222.
RX      MEDLINE=92375724; PubMed=1508712;
RA      Eguich Y., Ewert D.L., Tsujimoto Y.;
RT      "Isolation and characterization of the chicken bcl-2 gene: expression
RL      in a variety of tissues including lymphoid and neuronal organs in
RN      adult and embryo.";
RN      Nucleic Acids Res. 20:4187-4192(1992).
[3]
RP      PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.
RX      MEDLINE=92727291; PubMed=9115213;
RA      Ito T., Deng X., Carr B., May W.S. Jr.;
RT      "Bcl-2 phosphorylation required for anti-apoptosis function.";
RL      J. Biol. Chem. 272:11671-11673(1997).
[4]
RP      DEPHOSPHORYLATION BY PP2A.
RX      MEDLINE=99069407; PubMed=9852076;
RA      Deng X., Ito T., Carr B., Mumby B., May W.S. Jr.;
RT      "Reversible phosphorylation of Bcl2 following interleukin 3 or
RL      bryostatins 1 is mediated by direct interaction with protein
RT      phosphatase 2A*.";
RL      J. Biol. Chem. 273:34157-34163(1998).
CC      -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC      including factor-dependent lymphohematopoietic and neural cells.
CC      Regulates cell death by controlling the mitochondrial membrane
CC      permeability. Appears to function in a feedback loop system with
CC      caspases. Inhibits caspase activity either by preventing the
CC      release of cytochrome c from the mitochondria and/or by binding to
CC      the apoptosis-activating factor (APAF-1).
CC      -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC      Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC      domains, and is necessary for anti-apoptotic activity (By
CC      similarity). Also interacts with APAF-1 and RAf-1.

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RESULT 7			
ARI_XENLA			
ID	ARI_XENLA	STANDARD:	PRT: 228 AA.
AC	Q91827;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Apoptosis regulator RI (Xr) (Fragment).		
OS	Xenopus laevis (African Clawed frog).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;		
CC	Xenopodinae; Xenopus.		

RESULT	8	
BCLX_RAT		
ID	BCLX_RAT	STANDARD; PRt; 233 AA.
AC	P53563; 062678; P70614; P70613; Q62836; Q64087; Q64128;	
DT	01-OCT-1996 (Rel. 34, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	Apoptosis regulator Bcl-x.	
GN	BCL2L1 OR BCL2L OR BCLX.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 ON NCBI\_TaxID=10116;  
 RX [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).  
 RC TISSUE-Brain;  
 RA Michaelidis T.M.;  
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Brain;  
 RA Messelink S.L., David G.L., Choi S., Velluona M., Hardwick J.M.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).  
 RC TISSUE-Thymus;  
 RA MEDLINE=96278736; PubMed=8662675;  
 RX Shiralwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Ohta S.;  
 RT "An additional form of rat Bcl-x, Bcl-xbeta, generated by an  
 RT unspliced RNA, promotes apoptosis in promyeloid cells.";  
 RL J. Biol. Chem. 271:13258-13265(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).  
 RC STRAIN-Sprague-Dawley; TISSUE-Ovary;  
 RX MEDLINE=95129487; PubMed=7828536;  
 RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;  
 RT "Expression of members of the bcl-2 gene family in the immature rat  
 RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa  
 RT cell apoptosis is associated with decreased bax and constitutive  
 RT bcl-2 and bcl-xlong messenger ribonucleic acid levels.";  
 RL Endocrinology 136:232-241(1995).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=98010630; PubMed=9346936;  
 RA Artion M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,  
 RA Morikawa K.;  
 RT "Crystal structure of rat Bcl-XL. Implications for the function of  
 RT the bcl-2 protein family.";  
 RL J. Biol. Chem. 272:27886-27892(1997).  
 CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (By similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane. The bcl-x(S) and  
 CC Bcl-x(beta) isoforms promote apoptosis.  
 CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By  
 CC similarity). Heterodimerization with BAX does not seem to be  
 CC required for anti-apoptotic activity (By similarity).  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
 CC ENVELOPE (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: BCL-X(L) (SHOWN HERE), BCL-X(S)  
 CC AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS  
 CC SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE  
 CC OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT  
 CC DETECTABLE LEVEL OF BCL-X(S).  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
 CC The BH1 and BH2 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity (By similarity).  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X82537; CAA57886.1; -  
 DR EMBL: X82537; CAA57887.1; -  
 DR EMBL: U10579; AAA19257.1; -  
 DR EMBL: U72350; AAB17353.1; -  
 DR EMBL: U72349; AAB17352.1; -  
 DR EMBL: U34963; AAA7686.1; -  
 DR EMBL: S76513; AAC60702.1; ALT\_INIT.  
 DR EMBL: S78284; AAC60702.1; -  
 DR PDB: 1AF3; 07-JUL-97.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH4.  
 DR InterPro: IPR004725; BCL2\_reg.  
 DR Pfam: PF00452; BCL-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;  
 KW 3D-structure.  
 FT DOMAIN 4 24 BH4.  
 FT 86 100 BH3.  
 FT 129 148 BH1.  
 FT DOMAIN 180 195 BH2.  
 FT TRANSMEM 210 226 POTENTIAL.  
 FT VARSPPLIC 126 188 MISSING (IN ISOFORM BCL-X(S)).  
 FT VARSPPLIC 189 233 DTFVDLGNNAASRGQEEFNFMFLTGMTAVAGVLLGSL  
 FT IDYSGDIPGL (IN ISOFORM BCL-X(BETA)).  
 FT R -> Q (IN REF. 1).  
 FT F -> S (IN REF. 2).  
 FT A -> E (IN REF. 2).  
 FT I -> L (IN REF. 4).  
 FT A -> V (IN REF. 4).  
 FT F -> SS (IN REF. 4).  
 FT A -> T (IN REF. 4).  
 FT A -> P (IN REF. 4).  
 FT CONFLICT 199 199  
 FT CONFLICT 201 201  
 SQ SEQUENCE 233 AA; 26158 MW; 2B62B6C3864BC8F CRC64;  
 Query Match 12.2%; Score 107; DB 1; Length 233;  
 Best Local Similarity 17.0%; Pred. No. 0.0022;  
 Matches 33; Conservative 25; Mismatches 44; Indels 92; Gaps 4;  
 QY 21 SPTDELYAQAALGKREYVHARLLRAGLSWS-----APERASPA----- 59  
 DB 2 SOSNSELV-----DLSTKLSQKGYSMQSFQVEENRTPEAPETPERETPSAINGN 54  
 QY 60 PEGRLA----- 65  
 DB 55 PSMHLADSPAVNGATGSHSSIDAREVIMAAVKAOLRAGDEFFELRYRRAFSDLTSLHI 114  
 QY 66 -----EVCYVLLGLGITGKVVSLYSAGLAADVCAVROQPAVHVLVDCIGEFV 115  
 DB 115 TPGTAYQSFQEVVNEFLFDGVMNGRITVAFSFGCALVESYDKEMQVLVSRIASMATYL 174  
 QY 116 RKTATWTLRRRGV 129  
 DB 175 NDHLEPMIENGW 188  
 RESULT 9  
 BCLX\_CHICK  
 ID BCLX\_CHICK STANDARD; PRT; 229 AA.  
 AC 007816; 098908;  
 DT 01-FEB-1995 (Rel. 31, Created)

DT 01-NOV-1997 (Rel. 35, last sequence update)  
 DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE Apoptosis regulator Bcl-X.  
 GN BCL2L1 OR BCLX OR BCL-X.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NCBI\_TaxID=9031;  
 RN NCB1  
 RP SEQUENCE FROM N.A. (SHORT FORM).  
 RX MEDLINE=93364977; PubMed=8358789;  
 RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,  
 RA Turka L.A., Mao X., Nunez G., Thompson C.B.;  
 RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator  
 RT of apoptotic cell death.";  
 RL Cell 74:597-608(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A. (LONG FORM).  
 RC STRAIN=Hubbard White Mountain; TISSUE=Testis;  
 RX MEDLINE=97264485; PubMed=9110311;  
 RA Villagrosa X., Mezquita C., Mezquita J.;  
 RT "differential expression of bcl-2 and bcl-x during chicken  
 RT spermatogenesis.";  
 RL Mol. Reprod. Dev. 47:26-29(1997).  
 CC -1- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG  
 CC FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT  
 CC ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
 CC ENVELOPE (BY SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A  
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID  
 CC DEVELOPMENT.  
 CC -1- DOMAIN: BHL2 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC  
 CC FUNCTION. INTRACT BHL1 AND BHL2 DOMAINS ARE REQUIRED FOR ANTI-  
 CC APOPTOTIC ACTIVITY (BY SIMILARITY).  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BHL1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BHL2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BHL3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BHL4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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 CC -----  
 DR EMBL: Z23110; CAAB0657.1; -;  
 DR EMBL: U26645; AAB07677.1; -;  
 DR PIR: A47537; A47537.  
 DR HSSP: P53563; IAF3.  
 DR InterPro: IPR002475; BCL2 family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH.  
 DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BHL1; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BHL; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BHL1; 1.  
 DR PROSITE: PS01258; BHL2; 1.  
 DR PROSITE: PS01259; BHL3; 1.  
 DR PROSITE: PS01260; BHL4; 1.  
 DR PROSITE: PS50063; BHL4\_2; 1.  
 KM Apoptosis; Transmembrane; Alternative splicing.  
 FT DOMAIN 4 24 BHL.  
 FT 82 96 BHL3.  
 FT DOMAIN

FT DOMAIN 125 144 BHL.  
 FT DOMAIN 176 191 BH2.  
 FT TRANSMEM 206 223 POTENTIAL.  
 FT VARSPPLIC 185 229 ERRVDYGNNAAEELRKGQETNKMLLTGATVAGVLLGSL  
 FT LSRK -> VRLALP (IN SHORT ISOFORM).  
 SQ SEQUENCE 229 AA; 25733 MW; A97D3A4D04C0E9DA CRC64;  
 Query Match 12.0%; Score 105.5; DB 1; Length 229;  
 Best local Similarity 24.4%; Pred. No. 0.003;  
 Matches 31; Conservative 23; Mismatches 64; Indels 9; Gaps 2;  
 QY 4 LRSSVFPAEIMDFPSPDKELVAQAKALGSEYHARLLRAGLSWAPERPAPGR 63  
 DB 66 VHRSSLEVHEIVRASD-----VROALRDADGDEFELRYRRAFSDLTSLHTTPTNAVQ 117  
 QY 64 -LAEVCYVLLRLGITCKKYVSLYSVYAGLAIVDCVROQAPAMVIAVDCGFEYRKLATW 122  
 DB 118 SFEQVYVELPHDGVNMGRIVAFSPGALCVESYDKEMRVLVGRTVSMVTYTLTDHLPW 177  
 QY 123 LRRRGW 129  
 DB 178 IQENGW 184  
 Db 178 IQENGW 184  
 RESULT 10  
 ID BCLX\_MOUSE STANDARD; PRT; 233 AA.  
 AC 064373; 060657; 060658; 061338;  
 DT 01-NOV-1997 (Rel. 35, last sequence update)  
 DT 01-NOV-1997 (Rel. 35, last sequence update)  
 DE 15-JUN-2002 (Rel. 41, last annotation update)  
 DE Apoptosis regulator Bcl-X.  
 GN BCL2L1 OR BCL2L OR BCLX.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN NCB1  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=2M4B;  
 RA Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=95331139; PubMed=7607090;  
 RA Gonzalez-Garcia M., Perez-Ballester R., Ding L., Duan L., Boise L.H.,  
 RA Thompson C.B., Nunez G.;  
 RT "bcl-XL is the major bcl-x mRNA form expressed during murine  
 RT development and its product localizes to mitochondria.";  
 RL Development 120:3033-3042(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS X(L); X(S) AND X(DELTA-TM)).  
 RC TISSUE=Pre-B cell;  
 RX MEDLINE=95052604; PubMed=7963517;  
 RA Fang W., Rivard J.J., Mueller D.L., Behrens T.W.;  
 RT "Cloning and molecular characterization of mouse bcl-x in B and T  
 RT lymphocytes.";  
 RL J. Immunol. 153:4388-4396(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM X(BETA)).  
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;  
 RX MEDLINE=98051053; PubMed=9390687;  
 RA Yang X.-F., Weber G.F., Cantor H.;  
 RT "A novel Bcl-x isoform connected to the T cell receptor regulates  
 RT apoptosis in T cells.";  
 RL Immunity 7:629-639(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97289584; PubMed=9144489;  
 RA Grilloit D.A., Gonzalez-Garcia M., Ekheraie D., Duan L., Inohara N.,  
 RA Ohta S., Seidlin M.F., Nunez G.;  
 RT "Genomic organization, promoter region analysis, and chromosome

RT Localization of the mouse bcl-x gene.\*;  
 RL J. Immunol. 158:4750-4757(1997).  
 CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (By similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane. The Bcl-x(s)  
 CC isoform promotes apoptosis.  
 CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By  
 CC similarity). Heterodimerization with BAX does not seem to be  
 CC required for anti-apoptotic activity (By similarity).  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
 CC ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).  
 CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S),  
 CC BCL-X(BETA) AND BCL-X(DELTA-TM); ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE  
 CC BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA-  
 CC TM) EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES THAT HAVE BEEN  
 CC ACTIVATED.  
 CC -1- DEVELOPMENTAL STAGE: BCL-X(BETA) IS EXPRESSED IN BOTH EMBRYONAL AND  
 CC POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND IN  
 CC POSTNATAL TISSUES.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
 CC The BH1 and BH2 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis (By  
 CC similarity). The cleaved protein, lacking the BH4 domain, has pro-  
 CC apoptotic activity (By similarity).  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC  
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 CC  
 DR EMBL: X83574; CAA58557.1; -  
 DR EMBL: L35049; AAS51039.1; -  
 DR EMBL: L35048; AAS51040.1; -  
 DR EMBL: U10102; AAB82174.1; -  
 DR EMBL: U10101; AAB82173.1; -  
 DR EMBL: U10100; AAB82172.1; -  
 DR EMBL: U51279; AAC53460.1; -  
 DR EMBL: U78031; AAB96881.1; -  
 DR EMBL: U78030; AAB96881.1; JOINED.  
 DR HSSP: P53563; IAF3.  
 DR MGD: MGI:88139; Bcl2l.  
 DR InterPro: IPR002475; BCL2 family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR InterPro: IPR004723; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRfam: TIGR00865; bcl-2.1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS0063; BH4\_2; 1.  
 DR Apoptosis: Mitochondrion; Alternative splicing; Transmembrane.  
 FT DOMAIN 4 24 BH4.  
 FT DOMAIN 86 100 BH3.  
 FT DOMAIN 129 148 BH1.

FT DOMAIN 180 195 BH2.  
 FT TRASPMM 210 226 POTENTIAL.  
 FT VARSPLIC 126 188 MISSING (IN ISOFORM BCL-X(S)).  
 FT VARSPLIC 189 233 DFFVDLYGNNAAESRKGDFRFRNFWLTGAGVLLGSL  
 FT VARSPLIC 194 233 FSRK -> VRTTPLYCPPLACVSLCEHP (IN ISOFORM  
 FT VARSPLIC 194 233 BCL-X(BETA)).  
 FT VARSPLIC 194 233 LYGNNAAESRKGDFRFRNFWLTGAGVLLGSLFSR-  
 FT VARSPLIC 194 233 -> GHDCGCGSAGLTLLQSEVTRH (IN ISOFORM BCL-  
 FT VARSPLIC 194 233 X(DELTA-TM)).  
 SQ SEQUENCE 233 AA; 26132 MW; 24D2AC79887E072E CRC64;  
 Query Match 12.0%; Score 105; DB 1; Length 233;  
 Best Local Similarity 26.6%; Pred. No. 0.0034;  
 Matches 17; Conservative 15; Mismatches 32; Indels 0; Gaps 0;  
 QY 66 EVCVTLRLGRTWGVSLYSVAAGLAVDCVRQAPAMVHALVDCLGEFRKTLATLRR 125  
 DB 125 QVYNELFRGVWGHVAFVFGALCVESYKENVLYSRASMAATYLNHLEPWIOE 184  
 QY 126 RGGW 129  
 DB 185 NGCW 188  
 RESULT 11  
 BCLX\_PIG STANDARD; PRT; 233 AA.  
 AC 077737;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-x.  
 GN BCL2L1 OR BCL2L OR BCLX.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 OX NCBI\_Taxid=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99171363; PubMed=10072723;  
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;  
 RT "Quantification of cardioprotective gene expression in porcine  
 RT short-term hibernating myocardium";  
 RL J. Mol. Cell. Cardiol. 31:147-158(1999).  
 CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (By similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane.  
 CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By  
 CC similarity). Heterodimerization with BAX does not seem to be  
 CC required for anti-apoptotic activity (By similarity).  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
 CC ENVELOPE (By similarity).  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
 CC The BH1 and BH2 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis (By  
 CC similarity). The cleaved protein, lacking the BH4 domain, has pro-  
 CC apoptotic activity (By similarity).  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

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CC -----
DR EMBL: AJ001203; CAA04597.1; -
DR HSSP: 007817; 1MA2.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfam: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PS50063; BH4_2; 1.
DR Apoptosis: Mitochondrion; Transmembrane.
KW DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.
FT DOMAIN 180 195 BH2.
FT TRANSMEM 210 226 POTENTIAL.
SQ SEQUENCE 233 AA; 26061 MW; 18BF6FA0441912B2 CRC64;

Query Match 11.8%; Score 104; DB 1; Length 233;
Best Local Similarity 26.6%; Pred. No. 0 0043;
Matches 17; Conservative 15; Mismatches 32; Indels 0; Gaps 0;

OY 66 EVCTVILRLGITWGVKVSIVSVAAGLVDCVROAPAMVHALVDCGEFVKTLATWLR 125
Db 125 QVNLLEFRDGVNMGRIYAFSPGALCVESVDKEMQVLVSRIAMWMTYINDHLEPIQE 184
OY 126 RCGM 129
Db 185 NGGM 188

RESULT 12
BCL2_HUMAN
ID BCL2_HUMAN STANDARD: PRT; 233 AA.
AC 007817; 092976;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-x.
OS Homo sapiens (Human).
GN BCL2L1 OR BCL2L OR BCLX.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RX MEDLINE=93384977; Pubmed=8358789;
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT of apoptotic cell death.";
RL Cell 74:597-608(1993).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM BETA).
RA Inohara N., Ohta S.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RL [3]
RP MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.
RX MEDLINE=95372373; Pubmed=7644501;
RA Sedlak T.W., Oltvai Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,
RA Korsmeyer S.J.;
RT "Multiple Bcl-2 family members demonstrate selective dimerizations
RT with Bax.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).
RN [4]

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RP MUTAGENESIS OF BH1 AND BH2 DOMAINS.
RX MEDLINE=96170038; Pubmed=8596636;
RX Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,
RA Korsmeyer S.J.;
RT "Bax-independent inhibition of apoptosis by Bcl-XL.";
RL Nature 379:554-556(1996).
RN [5]
RP STRUCTURE BY NMR OF 1-209.
RX MEDLINE=97172562; Pubmed=9020082;
RA Sattler M., Liang H., Nettelsheim D., Meadows R.P., Harlan J.E.,
RA Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
RA Thompson C.B., Fesik S.W.;
RT "Structure of Bcl-XL-Bax peptide complex: recognition between
RT regulators of apoptosis.";
RL Science 275:983-986(1997).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.
RX MEDLINE=96256675; Pubmed=8692274;
RA Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,
RA Yoon H.S., Nettelsheim D., Chang B.S., Thompson C.B., Wong S.L.,
RA Ng S.L., Fesik S.W.;
RT "X-ray and NMR structure of human Bcl-XL, an inhibitor of programmed
RT cell death.";
RL Nature 381:335-341(1996).
RN [7]
RP CLEAVAGE BY CASPASES, AND MUTAGENESIS OF ASP-61.
RX MEDLINE=98118550; Pubmed=9435230;
RA Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.,
RA Takahashi A., Kastan M.B., Griffin D.E., Earnshaw W.C., Velliona M.A.,
RA Hardwick J.M.;
RT "Modulation of cell death by Bcl-XL through caspase interaction.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).
CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC caspases (By similarity). Appears to regulate cell death by
CC blocking the voltage-dependent anion channel (VDAC) by binding
CC to it and preventing the release of the caspase activator,
CC cytochrome c, from the mitochondrial membrane. The Bcl-x(s)
CC isoform promotes apoptosis.
CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2.
CC Heterodimerization with BAX does not seem to be required for anti-
CC apoptotic activity.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC ENVELOPE (By similarity).
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: BCL-X(L) (SHOWN HERE), BCL-X(S)
CC AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS
CC THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING
CC LYMPHOCTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING
CC LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization
CC with other Bcl2 family members and for repression of cell death.
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC
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CC
CC EMBL: Z23116; CAA80662.1; -
CC DR EMBL: Z23115; CAA80661.1; -
CC DR EMBL: U72396; AAB17354.1; -
CC DR PDB: 1BXI; 29-OCT-97.

```

PDB: 1XL; 21-APR-97.  
 DR PDB; 1MAZ; 21-APR-97.  
 DR Genew; HGNC:992; BCL2L1.  
 DR MIM; 600039; .  
 DR InterPro: IPR002475; BCL2 family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH.  
 DR InterPro: IPR004725; Bcl2\_Reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR TIGRFAMs; TIGR00865; bcl-2; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
 DR PROSITE; PS0063; BH4-2; 1.  
 DR Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;  
 KM 3D-structure.  
 FT DOMAIN 4 24  
 FT DOMAIN 86 100 BH4.  
 FT DOMAIN 129 148 BH1.  
 FT DOMAIN 180 195 BH2.  
 FT TRANSMEM 210 226  
 FT SITE 61 61  
 FT VARSPLIC 126 188  
 FT VARSPLIC 189 233  
 FT MUTAGEN 61 61  
 FT MUTAGEN 131 133  
 FT MUTAGEN 135 137  
 FT MUTAGEN 138 140  
 FT MUTAGEN 138 138  
 FT MUTAGEN 148 148  
 FT MUTAGEN 156 156  
 FT MUTAGEN 176 176  
 FT MUTAGEN 188 189  
 FT MUTAGEN 189 189  
 FT CONFLICT 70 70  
 FT SEQUENCE 233 AA; 26049 MW; E09D3CDD851AE9BE CRC64;  
 Query Match 11.7%; Score 103; DB 1; Length 233;  
 Best Local Similarity 26.6%; Pred. No. 0.0054;  
 Matches 17; Conservative 15; Mismatches 32; Indels 0; Gaps 0;  
 QY 66 EVCYVLLRLGRTGWKGVSLYSVAAGLAVDCVROAPAMVHALVDCLGFEVRLTLATWLR 125  
 DB 125 QVNLLEFRGVNMGRIYAFVFGALCVESVDKEMQVLVSRIAAWATYLNHLPEWIDE 184  
 QY 126 RGGW 129  
 DB 185 NGW 188  
 RESULT 13  
 BAXB\_HUMAN STANDARD; PRT; 218 AA.  
 AC Q07814;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator BAX, cytoplasmic isoform beta.  
 GN BAX.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-B-cell;  
 RX MEDLINE=93364978; PubMed=8358790;  
 RA Oliva Z.N., Millman C.L., Korsmeyer S.J.;  
 RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that  
 RT accelerates programmed cell death."  
 RL Cell 74:609-619(1993).  
 CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND  
 CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADONOVIRUS  
 CC HOMOLOG FLB 19K PROTEIN.  
 CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,  
 CC FLB 19K PROTEIN, BCL-X(L), MCL-1 AND A1.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE  
 CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY  
 CC ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  
 CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND  
 CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION  
 CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.  
 CC -1- SIMILARITY: CONTRAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTRAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; L22474; AAA03620.1; .  
 DR PIR; BA7538; B47538.  
 DR HSSP; Q07817; 1MAZ.  
 DR Genew; HGNC:959; BAX.  
 DR MIM; 600040; .  
 DR InterPro: IPR002475; BCL2 family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS0062; BCL2\_FAMILY; 1.  
 DR Apoptosis; Alternative splicing.  
 KM DOMAIN 59 73 BH3.  
 FT DOMAIN 98 118 BH1.  
 FT DOMAIN 150 165 BH2.  
 FT SEQUENCE 218 AA; 24220 MW; F69DCD70F960192F CRC64;  
 Query Match 11.5%; Score 101; DB 1; Length 218;  
 Best Local Similarity 22.2%; Pred. No. 0.0078;  
 Matches 34; Conservative 25; Mismatches 52; Indels 42; Gaps 5;  
 QY 22 PDKELVAQAKALGRE-VYHARLRLAGLSWSAPERA-SPAP-GRGLAEVCYVLLRLG--- 75  
 DB 13 PTSSQDIKKTGALLLQGIQDRAGRG--GEAPDLALDPVPODASTKISSELRKIGDEL 70  
 QY 76 -----ITWGRVSLYSVAAGLAVDCVROAP 101  
 DB 71 DSNMELQRMIAVDVDSREVEFRVAADMFSDGNFNMGWVALLFFASKLVLKALCTVNP 130  
 QY 102 AMVHALVDCLGFEVRLTLATWLRGGGTVDYK 134  
 DB 131 ELIRITMGWTLDFLRRLRLGWTIDOGGWVRLK 163  
 RESULT 14





Db 97 QVMGELFRDGTWGRIVAFSFGALCVESANKENTDLPRIYOMVNTLEHTLOPWOE 156  
.QY 126 RCGW 129  
111  
Db 157 NGGW 160

Search completed: April 29, 2003, 11:23:55  
Job time : 6.99217 secs

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GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:20:36 ; Search time 10.6527 seconds  
(without alignments)  
1534.145 Million cell updates/sec

Title: US-09-682-667-4

Perfect score: 878

Sequence: 1 MEVLRSSVFAEIMDAFDR.....TLCFGRFLKAFLLPER 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : PIR\_73:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	134	15.3	236	2	153744
2	130	14.8	239	1	TVH0A1
3	128.5	14.6	236	2	I67432
4	128	14.6	236	2	JC7383
5	127	14.5	236	1	TVMSA1
6	125	14.2	205	1	TVH0B1
7	124	14.1	199	1	TVMSB1
8	118	13.4	216	2	B37332
9	114	13.0	227	2	JEO203
10	113	12.9	233	2	A37332
11	106	12.1	233	2	S51761
12	105.5	12.0	190	2	A47537
13	105	12.0	214	2	I49057
14	105	12.0	233	2	I49056
15	104.5	11.9	232	2	S24390
16	103	11.7	233	2	B47537
17	101	11.5	218	2	B47538
18	100	11.2	233	2	I67431
19	98	11.2	179	2	JC7255
20	97	11.0	211	2	S58873
21	96	10.9	192	2	A47538
22	94	10.7	133	2	I53295
23	93.5	10.6	143	2	I38221
24	93	10.6	192	2	D47538
25	87	9.9	211	2	S58875
26	83.5	9.5	172	2	I49449
27	82.5	9.4	412	2	T37042
28	80.5	9.2	412	2	C82750
29	80	9.1	1115	2	A70990

30	79	9.0	401	1	A36961	pin biogenesis p
31	78.5	8.9	154	2	I58194	gene bcl-2 protein
32	78.5	8.9	320	2	C72629	hypothetical prote
33	78.5	8.9	419	2	A83133	probable MFS trans
34	78.5	8.9	540	2	T34702	hypothetical prote
35	78	8.9	175	2	I39055	Bcl-2 related - hu
36	78	8.9	212	2	S53257	e antigen precursor
37	77.5	8.8	373	2	H84404	ferichrome ABC tr
38	77.5	8.8	482	2	C86442	probable amino aci
39	77.5	8.8	822	2	AE2404	DNA helicase (limp
40	77.5	8.8	1010	2	AH2553	hypothetical prote
41	76.5	8.7	297	2	T46864	nicotinate-nucleot
42	76	8.7	333	2	C95368	hypothetical prote
43	76	8.7	356	2	G81907	probable integral
44	75.5	8.6	495	2	D86442	probable amino aci
45	75.5	8.6	610	2	T09988	probable transcrip

## ALIGNMENTS

## RESULT 1

I53744

gene bcl-2 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 16-Jul-1999

C:Accession: I53744

R/Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.

Gene 140, 291-292, 1994

A:Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.

A:Reference number: I53744; MUID:94193015; PMID:8144041

A:Accession: I53744

A:Status: preliminary; translated from GB/EMBL/DDU

A:Molecule type: mRNA

A:Residues: 1-236 <RES>

A:Cross-references: GB:I14680; MID:9408946; PIDN:AA53662.1; PID:9408947

A:Gene: bcl-2

C:Superfamily: bcl transforming protein

Query Match 15.3%; Score 134; DB 2; Length 236;

Best Local Similarity 20.5%; Pred. No. 7.7e-06;

Matches 45; Conservative 24; Mismatches 58; Indels 92; Gaps 5;

QY	28	VAQAKALG-----REYHARLLRAGLSV-----SAPERASAPAG-----	61
DB	1	MAQAGRTGYDNRREIVAKYIHVLSQRCYEMDTGDEDSAPLRAAPTEIFSFQPSNRTPA	60
QY	62	-----	61
DB	61	VHROTAARTSPRLPLVANNAGPALSPVPVYHLTLRRAGDDFSRRYRDRFAEMSSQLALTP	120
QY	62	-----GRLAEVCTVLLRLGITGWKRVSLYSVAAGLAVDCVQAOAPAMVHALVDCLEGFVRK	117
DB	121	FTARGRAATVVEELFRGVNMGRIVAFFEEFGVWCVSVRREMSPLVDNIALMTETYLNR	180
QY	118	TLATWLLRRRGWTDVLKCV-VSTDPGFRSHWL-VATICS 154	
DB	181	HLHTWIDNGMGDAFVELYGPSPMRPLFDFSWLSLKLTLIS 219	

## RESULT 2

TVH0A1

transforming protein bcl-2, splice form alpha - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1988 #sequence\_revision 07-Jun-1996 #text\_change 15-Oct-1999

C:Accession: C37332; A29409; S02452; A24428; A27622; B27622

R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a va

A:Reference number: A37332; MUID:92375724; PMID:1508712

A:Accession: C37332

A:Status: nucleic acid sequence not shown; not compared with conceptual translation



Db 181 HLHTWIQDNGMDAFVELYGPVSRPLEDFSMLSLTKTLLS 219

## RESULT 5

TVMSAI

transforming protein bcl-2-alpha - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 18-Jun-1999

C:Accession: A25960, E37332

R:Negri, M.; Sillini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.

Cell 49, 455-463, 1987

A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homolog

A:Reference number: A90893; MUID:87187643; PMID:3032455

A:Accession: A25960

A:Molecule type: DNA

A:Residues: 1-236 &lt;NEG&gt;

A:Cross-references: GB:LJ1532; GB:M16506; NID:q468336; PIDN:AAA37282.1; PID:q387109

R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety

A:Reference number: A37332; MUID:92375724; PMID:1508712

A:Accession: E37332

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: DNA

A:Residues: 1-33, 'E', '34-220', 'AL', '223-236' &lt;EGU&gt;

C:Genetics:

A:Gene: BCL2

A:Introns: 192/3

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane pro

Query Match 14.5%; Score 127; DB 1; Length 236;  
Best Local Similarity 19.6%; Pred. No. 3.9e-05;

Matches 43; Conservative 26; Mismatches 58; Indels 92; Gaps 5;

Db 28 VAQAKALG-----REYVHARLLRAGLSW-----SAPERASAPAG----- 61

1 MAQAGRGYDNRREIVMKYIHYKLSQRGYEWDADADAPGAPPTGIFSFQESNMPA 60

QY 62 ----- 61

Db 61 VHREMAARTSPLRLPVATAGPALSPPVPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTP 120

QY 62 ----GRLAEVCTVLLRLGITWGKVSLSYVAAGLAVDCVROAQPRAWHLVDDCGEFPVRK 117

Db 121 FTARGFAIVYEEFLFRDGVNMGRIVAFEEFGVWCYESVNRKMSPLVDNIALMWTETLNR 180

QY 118 TLATWLRRCGWTDLKCV-VSTDPGRSHML-VATLCS 154

Db 181 HLHTWIQDNGMDAFVELYGPVSRPLEDFSMLSLTKTLLS 219

RESULT 6

TVHDBI

transforming protein bcl-2; splice form beta - human

N:Alternate names: apoptosis regulator bcl-2

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 15-Oct-1999

C:Accession: B29409, I52566; D37332

R:Tsujimoto, Y.; Croce, C.M.

Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986

A:Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene

A:Reference number: A29409; MUID:86259760; PMID:3523487

A:Accession: B29409

A:Molecule type: mRNA

A:Residues: 1-205 &lt;TSU&gt;

A:Cross-references: GB:M13995; NID:q179368; PIDN:AAA51814.1; PID:q179369

R:Tanaka, S.; Louie, D.C.; Kant, J.A.; Reed, J.C.

Blood 79, 229-237, 1992

A:Title: Frequent incidence of somatic mutations in translocated BCL2 oncogenes of non-H

A:Reference number: I52566; MUID:92096610; PMID:1339299

A:Accession: I52566

A:Status: translated from GB/EMBL/DBU  
A:Molecule type: DNA

A:Residues: 1-131 <TAN>

A:Cross-references: GB:S72602; NID:q241046; PIDN:AAD14111.1; PID:q4261811

R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety

A:Reference number: A37332; MUID:92375724; PMID:1508712

A:Accession: D37332

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: DNA

A:Residues: 1-33, 'E', '34-95', 'T', '97-109', 'R', '111-205' <EGU>

C:Genetics:

A:Gene: BCL2

A:Cross-references: GDB:119031; OMIM:151430

A:Map position: 18q21.3-18q21.3

C:Function:

A:Description: blocks apoptosis in hematopoietic cells

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; pr

Query Match 14.2%; Score 125; DB 1; Length 205;  
Best Local Similarity 17.9%; Pred. No. 5.3e-05;

Matches 32; Conservative 22; Mismatches 39; Indels 86; Gaps 2;

Db 37 EYVHARLLRAGLSW-----SAPERASAPAG----- 61

Db 17 KYTHKYSQKGYEWDADGAVGAPGAPGATPCTSSQPGHTPHRASDPARTSPLOTPTA 76

QY 62 -----GRLAEVCTV 70

Db 77 APGAAGPALSPPVPHVHLRQAGDDFSRRYRGDFAEMSSQLHLTPFTARGFAIVYEE 136

QY 71 LRLGITWGKVSLSYVAAGLAVDCVROAQPRAWHLVDDCGEFPVRKTLATWLRRCGW 129

Db 137 LFRDGVNMGRIVAFEEFGVWCYESVNRKMSPLVDNIALMWTETLNLHLHTWIQDNGW 195

RESULT 7

TVMSBI

transforming protein bcl-2-beta - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 18-Jun-1999

C:Accession: B25960

R:Negri, M.; Sillini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.

Cell 49, 455-463, 1987

A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene ho

A:Reference number: A90893; MUID:87187643; PMID:3032455

A:Accession: B25960

A:Molecule type: DNA

A:Residues: 1-199 &lt;NEG&gt;

A:Cross-references: GB:M16506; NID:q468335; PIDN:AAA37281.1; PID:q387110

C:Genetics:

A:Gene: BCL2

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; transforming protein

Query Match 14.1%; Score 124; DB 1; Length 199;  
Best Local Similarity 19.0%; Pred. No. 6.4e-05;

Matches 38; Conservative 24; Mismatches 46; Indels 92; Gaps 4;

Db 28 VAQAKALG-----REYVHARLLRAGLSW-----SAPERASAPAG----- 61

1 MAQAGRGYDNRREIVMKYIHYKLSQRGYEWDADADAPGAPPTGIFSFQESNMPA 60

QY 62 ----- 61

Db 61 VHREMAARTSPLRLPVATAGPALSPPVPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTP 120

QY 62 ----GRLAEVCTVLLRLGITWGKVSLSYVAAGLAVDCVROAQPRAWHLVDDCGEFPVRK 117

Db 121 FTARGFAIVYEEFLFRDGVNMGRIVAFEEFGVWCYESVNRKMSPLVDNIALMWTETLNR 180





```

Db      7  RGYDNREIYL-----KYIHYKLSQRGYDWAAGEDRPVPAPAPAPAAVAAGASS 59
Oy      61  -----60
Db      60  HHRPSPAPALLVRCPRKNGCAAPGVHLLALROAGDEFSRRYQORDEFAQMSGOLHLPFTA 119
Oy      61  GGRLAEVCTVLLRLGITWGVVSLYSVAGLAVDCVROAPAMVHALVDCLGEFVRKTLA 120
Db      120  TGRFVAVVEELFRDGVNMVRIVAFEEFGVMCVESYNREMSPLVDNIATMTETELNRLH 179
Oy      121  TWLRRRGWTDVLCV-VSTDGFRSHW-----LVATLCSGRFL 159
Db      180  NMIDNGGMDAFVELYGNMRLPFDPSWISLKTILSLVLVGACITLGAYL 229

```

Search completed: April 29, 2003, 11:26:35  
 Job time : 12.6527 secs



GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2003, 11:16:46 ; Search time 25.9661 Seconds  
(without alignments)  
872.393 Million cell updates/sec

Title: US-09-682-667-4  
Perfect score: 878  
Sequence: 1 MEVLRSSVFPAEIMDAFDR.....TLCSPGRFLKAFILLPER 170

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq\_101002:\*

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*
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- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*
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- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	871	99.2	170	20	AAV14154
2	860	97.9	170	20	AAV14155
3	846.5	96.4	213	20	AAV14153
4	828.5	94.4	213	20	AAV14155
5	817.5	93.1	213	21	AAAB41444
6	495	56.4	134	22	AAAB56655
7	495	56.4	176	21	AAAB58949
8	173.5	19.8	247	22	ABB63760
9	173	19.7	846	22	ABB64401
10	131	14.9	239	17	AAW02383

11	131	14.9	239	22	AAAG64036	Human Bcl-2 protei
12	131	14.9	239	22	AAAG64038	Human Bcl-2 protei
13	130	14.8	239	9	AAAB09877	Sequence of bcl-2-
14	130	14.8	239	14	AAAR42312	Bcl-2 oncogene pro
15	130	14.8	239	16	AAAR70331	Human bcl-2 protei
16	130	14.8	239	16	AAAR71404	Human bcl-2 protei
17	130	14.8	239	19	AAAW40217	Human bcl-2. Homo
18	130	14.8	239	20	AAAB87810	A human Bcl-2 prot
19	130	14.8	239	20	AAAB87812	A human Bcl-2 alph
20	130	14.8	239	22	AAE08573	Human Bcl-2 protei
21	130	14.8	239	22	AAAG64035	Human Bcl-2 protei
22	130	14.8	239	22	AAAG64037	Human Bcl-2 protei
23	130	14.8	239	22	AAAB74127	Human bcl-2. Homo
24	130	14.8	239	22	AAAB74129	Human Bcl-2 protei
25	130	14.8	239	22	AAAB48288	Human Bcl-2 protei
26	130	14.8	239	22	AAAB35130	Human Bcl-2. Homo
27	130	14.8	239	22	AAAB50537	Human Bcl-2 protei
28	130	14.8	239	23	AAAB75986	Protein sequence.
29	130	14.8	239	23	AAU76553	Human Bcl-2 polyph
30	130	14.8	239	23	AAAB05227	Human D34A caspase
31	130	14.8	272	19	AAV21120	Human bcl2 proto-o
32	128	14.6	239	22	AAAG64039	Human Bcl-2 protei
33	127	14.5	229	17	AAW01021	Apoptosis-blocking
34	127	14.5	229	20	AAW94348	Human Bcl-2 mutant
35	127	14.5	236	20	AAW87811	A murine Bcl-2 pro
36	127	14.5	236	22	AAAB74128	Murine bcl-2. Mus
37	127	14.5	236	22	AAAB35131	Murine Bcl-2. Mus
38	127	14.5	236	23	AAU76554	Murine Bcl-2 polyph
39	127	14.5	239	15	AAAR47344	Human oncogene bcl
40	125.5	14.3	232	17	AAW01020	Apoptosis-blocking
41	125.5	14.3	232	20	AAW94347	Human Bcl-2 mutant
42	125	14.2	205	16	AAAR70332	Human bcl-2 protei
43	125	14.2	205	16	AAAB68886	Human thymus Bcl-2
44	125	14.2	205	16	AAAR71405	Human bcl-2 beta p
45	125	14.2	205	18	AAAB31529	Human anti-apoptot

## ALIGNMENTS

RESULT 1	AAV14154	
ID	AAV14154	standard; Protein; 170 AA.
XX		
AC	AAV14154;	
XX		
DT	27-JUL-1999	(first entry)
XX		
DE	Rat Bok protein sequence.	
XX		
KW	Bok protein; Bcl-2-related ovarian killer; BH31 variant; endometriosis;	
KW	pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;	
KW	reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;	
KW	ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;	
XX		
OS	Rattus rattus.	
XX		
PN	W09924453-A1.	
XX		
PD	20-MAY-1999.	
XX		
PF	04-NOV-1998;	98WO-US23523.
XX		
PR	07-NOV-1997;	97US-0064943.
XX		
PA	(STRD ) UNIV LELAND STANFORD JUNIOR.	
XX		
PI	Hsu SY, Hsueh AW;	
XX		
DR	WPI: 1999-327356/27.	
XX		
DR	N-PSDB; AAX61104.	
XX		

PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
 PT protein and its related gene

PS Claim 2; Page 54-55; 62pp; English.

CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
 CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
 CC pro-apoptotic Bok-related protein can be introduced into cell populations  
 CC to upregulate expression of the proteins in order to induce apoptosis in  
 CC the cell population. This is useful for treatment of diseases where there  
 CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
 CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
 CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
 CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
 CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
 CC other tissues, and provide a means for manipulating apoptosis. The Bok  
 CC protein and transgenic animal are also useful for identifying ligands or  
 CC substrates. Modulation of the gene activity in vivo is useful for  
 CC prophylaxis and therapy of, e.g. cancer and other proliferative  
 CC disorders. Bok genes are also useful for identification of cell type  
 CC based on expression. Identification of Bok as a new pro-apoptotic protein  
 CC with wide tissue distribution and heterodimerisation properties  
 CC facilitates elucidation of apoptosis mechanisms.

CC Sequence 170 AA;

Query Match 99.2%; Score 871; DB 20; Length 170;

Best Local Similarity 99.4%; Pred. No. 7.3e-93;

Matches 169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MEVLRSSVFPAEIMDADRSPTDKELVAQAALGREYVHARLRAGLSWSAPERASPAP 60  
 DB 1 MEVLRSSVFPAEIMDADRSPTDKELVAQAALGREYVHARLRAGLSWSAPERASPAP 60  
 OY 61 GGRLAEEVCTVLLRLGITMGKVVSLYSVAAGLAVDCVROAOPAMVHALVDCLEEFYRKTLA 120  
 DB 61 GGRLAEEVCTVLLRLGITMGKVVSLYSVAAGLAVDCVROAOPAMVHALVDCLEEFYRKTLA 120  
 OY 121 TWLRRGGWTDVLCVSTDPGFRSHMLVATLCSPGRFLKAAFLLPBER 170  
 DB 121 TWLRRGGWTDVLCVSTDPGFRSHMLVATLCSPGRFLKAAFLLPBER 170

RESULT 2

ID AAY14156 standard; Protein: 170 AA.

AC AAY14156;

DT 27-JUL-1999 (first entry)

XX Human Bok protein sequence.

DE Bok protein; Bcl-2-related ovarian killer; BH3 variant; endometriosis;  
 KW pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
 KW reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
 KW ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
 KW proliferative disorder; human.

XX Homo sapiens.

OS WO9924453-A1.

PN 20-MAY-1999.

PD 04-NOV-1998; 98WO-US23523.

PR 07-NOV-1997; 97US-0064943.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

PR Hsu SY, Hsueh AJW;

XX

DR WPI: 1999-327356/27.

DR N-PSDB: AAX61106.

PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
 PT protein and its related gene

PS Claim 2; Page 57-58; 62pp; English.

CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
 CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
 CC pro-apoptotic Bok-related protein can be introduced into cell populations  
 CC to upregulate expression of the proteins in order to induce apoptosis in  
 CC the cell population. This is useful for treatment of diseases where there  
 CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
 CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
 CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
 CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
 CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
 CC other tissues, and provide a means for manipulating apoptosis. The Bok  
 CC protein and transgenic animal are also useful for identifying ligands or  
 CC substrates. Modulation of the gene activity in vivo is useful for  
 CC prophylaxis and therapy of, e.g. cancer and other proliferative  
 CC disorders. Bok genes are also useful for identification of cell type  
 CC based on expression. Identification of Bok as a new pro-apoptotic protein  
 CC with wide tissue distribution and heterodimerisation properties  
 CC facilitates elucidation of apoptosis mechanisms.

CC Sequence 170 AA;

Query Match 97.9%; Score 860; DB 20; Length 170;

Best Local Similarity 98.2%; Pred. No. 1.4e-91;

Matches 167; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 MEVLRSSVFPAEIMDADRSPTDKELVAQAALGREYVHARLRAGLSWSAPERASPAP 60  
 DB 1 MEVLRSSVFPAEIMDADRSPTDKELVAQAALGREYVHARLRAGLSWSAPERASPAP 60  
 OY 61 GGRLAEEVCTVLLRLGITMGKVVSLYSVAAGLAVDCVROAOPAMVHALVDCLEEFYRKTLA 120  
 DB 61 GGRLAEEVCTVLLRLGITMGKVVSLYSVAAGLAVDCVROAOPAMVHALVDCLEEFYRKTLA 120  
 OY 121 TWLRRGGWTDVLCVSTDPGFRSHMLVATLCSPGRFLKAAFLLPBER 170  
 DB 121 TWLRRGGWTDVLCVSTDPGFRSHMLVATLCSPGRFLKAAFLLPBER 170

RESULT 3

ID AAY14153 standard; Protein: 213 AA.

AC AAY14153;

DT 27-JUL-1999 (first entry)

XX Rat Bok protein sequence.

DE Rat Bok protein; Bcl-2-related ovarian killer; BH3 variant; endometriosis;  
 KW pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
 KW reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
 KW ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
 KW proliferative disorder; rat.

XX Rattus rattus.

OS WO9924453-A1.

PN 20-MAY-1999.

PD 04-NOV-1998; 98WO-US23523.

PR 07-NOV-1997; 97US-0064943.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Hsu SY, Hsueh AJW;  
 XX  
 DR WPI: 1999-327356/27.  
 DR N-PSDB; AAX61103.  
 XX  
 PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
 PT protein and its related gene  
 XX  
 PS Claim 2: Page 53-54; 62pp; English.  
 XX  
 CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
 CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
 CC pro-apoptotic Bok-related protein can be introduced into cell populations  
 CC to upregulate expression of the proteins in order to induce apoptosis in  
 CC the cell population. This is useful for treatment of diseases where there  
 CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
 CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
 CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
 CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
 CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
 CC other tissues, and provide a means for manipulating apoptosis. The Bok  
 CC protein and transgenic animal are also useful for identifying ligands or  
 CC substrates. Modulation of the gene activity in vivo is useful for  
 CC prophylaxis and therapy of, e.g. cancer and other proliferative  
 CC disorders. Bok genes are also useful for identification of cell type  
 CC based on expression. Identification of Bok as a new pro-apoptotic protein  
 CC with wide tissue distribution and heterodimerisation properties  
 CC facilitates elucidation of apoptosis mechanisms.  
 CC  
 XX Sequence 213 AA;  
 SQ  
 Query Match 96.4%; Score 846.5; DB 20; Length 213;  
 Best Local Similarity 79.8%; Pred. No. 6.9e-90;  
 Matches 170; Conservative 0; Mismatches 0; Indels 43; Gaps 1;  
 QY 1 MEVLRSSVFAEIMDAFDRSPDKELVAQAKALGREYVHARLLRAGLSNAPERASAP 60  
 DB 1 MEVLRSSVFAEIMDAFDRSPDKELVAQAKALGREYVHARLLRAGLSNAPERASAP 60  
 QY 61 GGRLAECVTLRL-----GTT 77  
 DB 61 GGRLAECVTLRLGDELQIRPSVYRNVARQLHIPLOSEPVTDAFLAVAGHIFSAGIT 120  
 QY 78 WCKVSVLSYSAAGLAVDCVQAOPAMVHALVDCLGFEVRRKTLATWLRRRGWTDLKCV 137  
 DB 121 WCKVSVLSYSAAGLAVDCVQAOPAMVHALVDCLGFEVRRKTLATWLRRRGWTDLKCV 180  
 QY 138 STDGFRSHWLVAATLCSFGRLKAFFLLPER 170  
 DB 181 STDGFRSHWLVAATLCSFGRLKAFFLLPER 213  
 RESULT 4  
 ID AAY14155 standard; Protein; 213 AA.  
 XX  
 AC AAY14155;  
 XX  
 DT 27-JUL-1999 (first entry)  
 XX  
 DE Human Bok protein sequence.  
 XX  
 KW Bok protein; Bcl-2-related ovarian killer; BH3 variant; endometriosis;  
 KW pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
 KW reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
 KW ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
 KW proliferative disorder; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Homo sapiens.  
 XX  
 PN WO924453-A1.  
 XX

PD 20-MAY-1999.  
 XX  
 PE 04-NOV-1998; 98WO-US23523.  
 XX  
 PR 07-NOV-1997; 97US-0064943.  
 XX  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX  
 PI Hsu SY, Hsueh AJW;  
 XX  
 DR WPI: 1999-327356/27.  
 DR N-PSDB; AAX61105.  
 XX  
 PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
 PT protein and its related gene  
 XX  
 PS Claim 2: Page 55-56; 62pp; English.  
 XX  
 CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
 CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
 CC pro-apoptotic Bok-related protein can be introduced into cell populations  
 CC to upregulate expression of the proteins in order to induce apoptosis in  
 CC the cell population. This is useful for treatment of diseases where there  
 CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
 CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
 CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
 CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
 CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
 CC other tissues, and provide a means for manipulating apoptosis. The Bok  
 CC protein and transgenic animal are also useful for identifying ligands or  
 CC substrates. Modulation of the gene activity in vivo is useful for  
 CC prophylaxis and therapy of, e.g. cancer and other proliferative  
 CC disorders. Bok genes are also useful for identification of cell type  
 CC based on expression. Identification of Bok as a new pro-apoptotic protein  
 CC with wide tissue distribution and heterodimerisation properties  
 CC facilitates elucidation of apoptosis mechanisms.  
 CC  
 XX Sequence 213 AA;  
 SQ  
 Query Match 94.4%; Score 828.5; DB 20; Length 213;  
 Best Local Similarity 78.4%; Pred. No. 8.5e-88;  
 Matches 167; Conservative 0; Mismatches 3; Indels 43; Gaps 1;  
 QY 1 MEVLRSSVFAEIMDAFDRSPDKELVAQAKALGREYVHARLLRAGLSNAPERASAP 60  
 DB 1 MEVLRSSVFAEIMDAFDRSPDKELVAQAKALGREYVHARLLRAGLSNAPERASAP 60  
 QY 61 GGRLAECVTLRL-----GTT 77  
 DB 61 GGRLAECVTLRLGDELQIRPSVYRNVARQLHIPLOSEPVTDAFLAVAGHIFSAGIT 120  
 QY 78 WCKVSVLSYSAAGLAVDCVQAOPAMVHALVDCLGFEVRRKTLATWLRRRGWTDLKCV 137  
 DB 121 WCKVSVLSYSAAGLAVDCVQAOPAMVHALVDCLGFEVRRKTLATWLRRRGWTDLKCV 180  
 QY 138 STDGFRSHWLVAATLCSFGRLKAFFLLPER 170  
 DB 181 STDGFRSHWLVAATLCSFGRLKAFFLLPER 213  
 RESULT 5  
 ID AAB41444 standard; Protein; 213 AA.  
 XX  
 AC AAB41444;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Human ORFX ORF1208 polypeptide sequence SEQ ID NO:2416.  
 XX  
 KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
 KW vulnery; antiproliferative; antiparkinsonian; neuroprotective;  
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiac;

KW Immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antinflammatory;  
KW antiviral; antibacterial; antifungal; antineumatic; antihypertoid;  
KW antinaemic; gene therapy; cancer; proliferative disorder; hypertension;  
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
KW cholesterol ester storage; systemic lupus erythematosus; infection;  
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KW bone damage; cartilage damage; antinflammatory disease; coagulation;  
KW thrombosis; contraceptive.

OS Homo sapiens.  
XX  
XX WO200058473-A2.  
XX  
XX  
XX 05-OCT-2000.  
XX  
XX 31-MAR-2000; 2000WO-US08621.  
XX  
XX 31-MAR-1999; 99US-0127607.  
XX 02-APR-1999; 99US-0127636.  
XX 05-APR-1999; 99US-0127728.  
XX 30-MAR-2000; 2000US-0540763.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shinkets RA, Leach M;  
XX  
XX WPI: 2000-602362/57.  
XX N-PSDB: AAC75653.  
XX  
XX Novel nucleic acids and peptides derived from open reading frame X,  
XX useful for treating e.g. cancers, proliferative disorders,  
XX neurodegenerative disorders and cardiovascular disease -  
XX  
XX  
XX Claim 11; Page 1750-1751; 5507pp; English.

CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
CC which represent the human OREF open reading frames 1 to 3161. The OREF  
CC sequences have activities such as: cytostatic; hepatotropic; vulnery;  
CC antiproliferative; antiparkinsonian; nootropic; neuroprotective;  
CC osteoplastic; anticonvulsant; antiarthritic; immunosuppressive;  
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;  
CC antidiabetic; hypotensive; dermatological; immunosuppressive;  
CC antinflammatory; antibacterial; antiviral; antifungal; antineumatic;  
CC antihypertoid; and antinaemic. The sequences can be used for determining  
CC the presence of or predisposition to, or preventing or treating  
CC pathological conditions associated with an OREF-associated disorder. The  
CC nucleic acids can be used to express OREF proteins in gene therapy  
CC vectors. The proteins and nucleic acids may be used to treat cancers,  
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
CC nocturnal haemoglobinuria, antinflammatory disease; to enhance  
CC coagulation; to inhibit thrombosis; and as a contraceptive.

SO Sequence 213 AA;  
XX  
XX

Query Match 93.1%; Score 817.5; DB 21; Length 213;  
Best Local Similarity 77.0%; Pred. No. 1.6e-86;  
Matches 164; Conservative 2; Mismatches 4; Indels 43; Gaps 1;

OY 1 MEVLRSSVFAEIMDADRSPTDKEIYAOKALGREGVHARLLRAGISWSPERASAP 60  
DB 1 MEVLRSSVFAEIMDADRSPTDKEIYAOKALGREGVHARLLRAGISWSPERASAP 60  
OY 61 GGRLAECVCTVLLRL-----GTT 77  
DB 61 GGRLAECVCTVLLRLGDELEMTIRPSYRNVARQIHTISLQSEPVYTAFLAVAGHITSAGIT 120

OY 78 WGVVSLYSVAGLAVDCVRQAQAPAMVHALVDCIGEEFVKTLATWLRGGTDTLKCVCV 137  
DB 121 WGVVSLYVAGLAVDCVRQAQAPAMVHALVDCIGEEFVKTLATWLRGGTDTLKCVCV 180  
OY 138 STDPEGRSHMLVATICSGRFLKAPFLLDPER 170  
DB 181 STDPEGRSHMLVATICSGRFLKAPFLLDPER 213

RESULT 6  
AAB85665  
ID AAB85665 standard; Protein; 134 AA.  
XX  
XX AAB85665;  
XX  
XX 29-OCT-2001 (first entry)  
XX  
XX Human Bcl-2-like polypeptide (clone HHEH17).  
XX  
XX Bcl-2-like polypeptide; autoimmune disorder; allergy; immunomodulatory;  
XX respiratory; cardiovascular; antiarthritic; immunostimulant; vaccine;  
XX immunosuppressive; antinflammatory; gene therapy.  
XX  
XX Homo sapiens.  
XX  
XX WO200157060-A1.  
XX  
XX 09-AUG-2001.  
XX  
XX 31-JAN-2001; 2001WO-US03080.  
XX  
XX 01-FEB-2000; 2000US-0179487.  
XX 07-FEB-2000; 2000US-0180697.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Ruben SM, Duan DR, Ni J;  
XX  
XX WPI: 2001-476279/51.  
XX N-PSDB: AAH47021.  
XX  
XX Nucleic acids encoding human Bcl-2-like polypeptides, useful for  
XX preventing, diagnosing and/or treating -  
XX  
XX  
XX Claim 12; Page 277-278; 285pp; English.

PS The invention provides nucleic acid molecules (NAM1) encoding 4 human  
CC Bcl-2-like polypeptides (PEP1). The NAM1 and PEP1 may be used in the  
CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate Bcl-2-like polypeptides' expression. The NAM1 may be used  
CC to produce the soluble Bcl-2-like polypeptides by standard recombinant  
CC methodology. The polypeptides may also be used as antigens in the  
CC production of antibodies against Bcl-2 and in assays to identify  
CC modulators of Bcl-2 expression and activity. The anti-Bcl-2 antibodies  
CC and antagonists may be used to down regulate expression and activity.  
CC The anti-PEP1 antibodies may also be used as diagnostic agents for  
CC detecting the presence of Bcl-2 polyps in samples (e.g. by enzyme linked  
CC immunosorbent assay (ELISA)). Disorders that may be prevented, diagnosed  
CC and/or treated by the above methods include, immunodeficiencies (e.g.  
CC a gammaglobulinemia and B cell lymphoproliferative disorder), autoimmune  
CC disorders (e.g. Rheumatoid arthritis and Grave's disease), allergic  
CC reactions, inflammations, respiratory diseases and cardiovascular  
CC disorders (a full list of disorders is given in the specification). The  
CC present sequence represents a human Bcl-2-like polypeptide.

SO Sequence 134 AA;  
XX  
XX

Query Match 56.4%; Score 495; DB 22; Length 134;  
Best Local Similarity 75.4%; Pred. No. 2.4e-49;  
Matches 98; Conservative 5; Mismatches 21; Indels 6; Gaps 1;

OY 41 ARLLRAGISWSPERASAPGRLAECVCTVLLRLGTTGKVVSLYSVAGLAVDCVRQAQ 100

Db 11 AROLHLSL-----QSEPVVTDALFLAVAGHIFSAGITWKGKVSLSVAAAGLADVCRQAQ 64  
 QY 101 PAMVHALVDCIGFEFVKRTLATWLRRGWTDVLCVSTDPGFRSHMLVATLCSFGRFLK 160  
 Db 65 PAMVHALVDCIGFEFVKRTLATWLRRGWTDVLCVSTDPGFRSHMLVATLCSFGRFLK 124  
 QY 161 AAFELLPPER 170  
 Db 125 AAFVLLPPER 134

RESULT 7  
 AAB58949  
 ID AAB58949 standard; Protein; 176 AA.  
 AC AAB58949;  
 XX  
 XX  
 DT 27-MAR-2001 (first entry)  
 XX  
 DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 657.  
 XX  
 KM Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;  
 KM neutropenic; neuroprotective; antiviral; anti-allergic; hepatotropic;  
 KM antidiabetic; anti-inflammatory; antilucer; vulnerary; anticonvulsant;  
 KM antibacterial; antifungal; antiparasitic; cardiant; immune disorder;  
 KM Addison's disease; allergy; autoimmune haemolytic anaemia;  
 KM autoimmune thyroiditis; diabetes mellitus; Crohn's disease;  
 KM multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
 KM cardiovascular disorder; wound healing; neurological disease.  
 KM  
 OS Homo sapiens.  
 XX  
 PN WO20055173-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US05881.  
 XX  
 PR 12-MAR-1999; 99US-0124270.  
 XX  
 PA (HUMA-) HUMAN.GENOME SCI INC.  
 PI Rosen CA, Ruben SM;  
 DR MPI: 2000-611515/58.  
 DR N-PSDB: AAF21852.  
 XX  
 PT New human breast and ovarian cancer associated gene sequences and the  
 PT polypeptides encoded by these genes, useful in the prevention,  
 PT treatment and diagnosis of cancer, immune disorders, cardiovascular  
 PT disorders and neurological diseases -  
 XX  
 PS Claim 11; Page 1103; 1299pp; English.  
 XX  
 CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human  
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are  
 CC associated with breast and ovarian cancer. Included in the invention are  
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the  
 CC isolation and characterisation of the DNA and protein sequences of the  
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist  
 CC or antagonist sequences exhibit cytostatic; immunosuppressive;  
 CC neutropenic; neuroprotective; antiviral; anti-allergic; hepatotropic;  
 CC antidiabetic; anti-inflammatory; antilucer; vulnerary; anticonvulsant;  
 CC antibacterial; antifungal; antiparasitic and cardiant activity. The  
 CC polynucleotide and protein sequences are used in the diagnosis of cancer,  
 CC particularly breast and ovarian cancer. The nucleic acid sequences,  
 CC proteins, agonists and antagonists may also be used in the diagnosis,  
 CC prevention and treatment of immune disorders e.g. Addison's disease,  
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,  
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid  
 CC arthritis and ulcerative colitis; cardiovascular disorders such as  
 CC myocardial ischaemias; wound healing; neurological diseases such as

CC cerebral anoxia and epilepsy; and infectious diseases.  
 XX  
 SQ Sequence 176 AA:  
 QY 41 ARLLRGLSWSAPERSAPAGRLAFCVTLRLGLTGWKVSLSVAAAGLADVCRQAQ 100  
 Db 53 AROLHLSL-----QSEPVVTDALFLAVAGHIFSAGITWKGKVSLSVAAAGLADVCRQAQ 106  
 QY 101 PAMVHALVDCIGFEFVKRTLATWLRRGWTDVLCVSTDPGFRSHMLVATLCSFGRFLK 160  
 Db 107 PAMVHALVDCIGFEFVKRTLATWLRRGWTDVLCVSTDPGFRSHMLVATLCSFGRFLK 166  
 QY 161 AAFELLPPER 170  
 Db 167 AAFVLLPPER 176

RESULT 8  
 ABB63760  
 ID ABB63760 standard; Protein; 247 AA.  
 AC ABB63760;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 18072.  
 XX  
 KM Drosophila; developmental biology; cell signalling; insecticide;  
 KM pharmaceutical.  
 KM  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 DR MPI: 2001-656860/75.  
 DR N-PSDB: ABL07863.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 PS Disclosure: SEQ ID NO 18072; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (AAB57737-ABR72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/Published\_pct\_sequences.  
 XX  
 SQ Sequence 247 AA:  
 Query Match 56.4%; Score 495; DB 21; Length 176;  
 Best Local Similarity 75.4%; Pred. No. 3.4e-49;  
 Matches 98; Conservative 5; Mismatches 21; Indels 6; Gaps 1;

Query Match 19.8%; Score 173.5; DB 22; Length 247;

	Best Local Similarity	27.8%; Pred.No.1.le=11;	Matches	44; Conservative	20; Mismatches	41; Incls	53; Gaps	4.
OY	25 KEIYAQAALGREYHARLRAGL-----SWSAP-----	53						
Dd	87 ODIIQGRCLGCHYIKRRRSGRLGIQRIRSLIGSTMGIVRDVFPAYVLDEL	146						
OY	54 ERASPA-----PGGR-----LAECYTLLRLGTGWKVSLSVAAGL	91						
Dd	147 ERMHRPIRYNGVARQICRNDBGFEHTPDAAVSLLGAVGRELFREVEITWKSVISLIAMGL	206						
OY	92 AVDCVRQAOAPAVALVDLCIGFVKTLATWLRRRGW	129						
Dd	207 SVDCVRQGHPETLPKLMSVSEVIDELVPWNENGW	244						

XX	Sequence	846 AA;
XX		
CC	The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.	
CC	(ABB57737-ABB72072).	
CC	sequences (ABL01840-ABL16175) and the encoded proteins	
CC	discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA	
CC	insecticides, therapeutics and pharmaceutical drugs. The invention	
CC	of cell-cell interactions in higher eukaryotes for the development of	
CC	useful in developmental biology and in elucidating cell signalling and	
CC	capable of detecting 1000 or more genes from Drosophila. The invention is	
CC	The invention relates to an isolated nucleic acid detection reagent	
XX		
PS	Disclosure; SEQ ID NO 19995; 21pp + Sequence Listing; English.	
PA	(PEKE ) PE CORP NY.	
PR	11-JUL-2000; 2000US-0614150.	
PR	23-MAR-2000; 2000US-191637P.	
PP	23-MAR-2001; 2001WO-US09231.	
PD	27-SEP-2001.	
PN	WO200171042-A2.	
OS	Drosophila melanogaster.	
XX		
XX	pharmaceutical.	
KW	Drosophila; developmental biology; cell signalling; insecticide;	
RW	Drosophila; developmental biology; cell signalling; insecticide;	
DE	Drosophila melanogaster polypeptide SEQ ID NO 19995.	
XX		
DT	26-MAR-2002 (first entry)	
AC	ABB64401;	
XX		
XX	ABB64401 standard; Protein; 846 AA.	
ID	ABB64401	
RESULT 9		

Query Match	19.7%	Score 173;	DB 22;	Length 846;
Best Local Similarity	28.2%	Pred. NO. 6.3e-11;		
Matches 44;	Conservative 17;	Mismatches 43;	Indels 52;	Gaps 3;
QY	26	ELVQAKALGREYVHARLLRAG-LSMSAPER	-----	55
	:::	:::	:	:

[illegible]

AA	RESULT	10
AAW02383		
ID	AAW02383	standard; Protein; 239 AA.
XX		
AC	AAW02383;	
XX		
D7	04-JUN-1997	(first entry)
XX		
DE	Human BCL2.	
XX		
KW	Sense oriented; genetic suppressor element; GSE; reverse;	
KW	BCL2; gene; mediated; suppression; apoptosis; mammalian; cell;	
KW	inhibition; sensitisation; cancer; chemotherapeutic agent;	
KW	increase; treatment; induction; virus; interference; death;	
KW	disease; haematopoietic; neurological; recombinant construct;	
KW	decrease; expression; anticancer; non-Hodgkin's lymphoma;	
KW	B cell malignancy.	

OS Homo sapiens.  
XX  
PN MO9629403-A1.  
XX  
PD 26-SEP-1996.  
XX  
PF 14-MAR-1996; 96WO-US03545.  
XX  
PR 17-MAR-1995; 95US-0405702.  
XX  
PA (UNII ) UNIV ILLINOIS FOUND.  
XX  
PI Holzmayner TA, Roninson IB, Schott B, Tarasewicz DG;  
XX  
DR WPI: 1996-443179/44.  
DR N-PSDB; AAT33694.  
XX  
PT Sense oriented genetic suppressor element - for reversing BCL2  
PT mediated inhibition of apoptosis, and for sensitizing cancer cells  
PT against chemotherapeutic agents  
XX  
DS Claim 20; Pages 37-38; 66pp; English.

CC The present invention is human BCL2 from which a peptide  
CC capable of inhibiting BCL2 gene, or gene product, function in a  
CC cell can be derived. The cDNA sequence encoding the peptide is a  
CC sense oriented genetic suppressor element (GSE) for reversing  
CC BCL2 mediated suppression of apoptosis in a mammalian cell. The  
CC GSE and its peptide product can be used to sensitize cancer cells  
CC to chemotherapeutic agents, and to increase apoptosis, especially  
CC for the treatment of cancer, but more generally to induce virus  
CC infected cell death, or to treat apoptosis related diseases of  
CC haematopoietic or neurological cells. The GSE peptide product or a  
CC recombinant construct encoding the GSE can be used to decrease  
CC BCL2 gene expression by exerting an anticancer effect, e.g. in  
CC cases of non-Hodgkin's lymphoma and B cell malignancy.

```

0Y      37 EYVHARLLRAGLSW-----SAPESPAPG----- 61
Query Match      14.9%; Score 131; DB 17; Length 239;
Best Local Similarity 19.4%; Pred. No. 9e-07;
Matches 40; Conservative 26; Mismatches 52; Indels 88; Gaps 4;

```

```

Db      17 KIHYKLSQRYGEMDAGVGAAPGGAAPAGIFSSQPGHTPHPAASRDVPARTSPLOTPA 76
QY      62 -----GRLAEVCTV 70
Db      77 APCGAAGPALSPVPVPHALALROAGDPSRRYRGDAEMSSOLHLPTTARGRFATVVEE 136
QY      71 LRLGITMGKVVSLYSVAAGLAVDCVROAPAMVHALVDCLGFEVFKTLATWLRRGGMT 130
Db      137 LFRDGVNMGRIYAFEFEGGVMSESVNREMSPLVDNIALMTEYLNRHLHTWIDNGMD 196
QY      131 DVLKCV-VSTDGFRSHWL-VATLCS 154
Db      197 AFVELYGPMSRPLDFDSWLSLTKTLIS 222

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## RESULT 11

```

AAG64036
ID      AAG64036 standard; protein; 239 AA.
XX
AC      AAG64036;
XX
DT      10-SEP-2001 (first entry)
XX
DE      Human Bcl-2 protein mutant #1.
XX
KW      Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
PN      WO200142459-A1.
XX
PD      14-JUN-2001.
XX
PF      07-DEC-2000; 2000MO-JP08667.
XX
PR      09-DEC-1999; 99JP-0350427.
XX
PA      (HISM ) HISAMITSU PHARM CO LTD.
XX
PI      Shlbazaki F, Kuma H;
XX
DR      WPI; 2001-381681/40.
XX
PT      New apoptosis inhibitors, useful for treating apoptosis related
XX      disorders -
XX
PS      Claim 5; Page 30-31; 43pp; Japanese.
XX
CC      The invention relates to an apoptosis inhibitor comprising the
CC      amino acid sequence of Bcl-2 protein in which at least one serine
CC      residue is substituted by alanine or aspartic acid. The protein has
CC      increased apoptosis inhibitory activity compared with the wild type
CC      Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment
CC      of disorders caused by apoptosis. The present sequence is a mutant
CC      Bcl-2 protein of the invention.
XX
SQ      Sequence 239 AA;

```

Query Match 14.9%; Score 131; DB 22; Length 239;

Best Local Similarity 19.4%; Pred. No. 9e-07;

Matches 40; Conservative 25; Mismatches 53; Indels 88; Gaps 4;

```

QY      37 EYVHARLLRAGLSM-----SAPERASAPAG----- 61
Db      17 KIHYKLSQRYGEMDAGVGAAPGGAAPAGIFSSQPGHTPHPAASRDVPARTSPLOTPA 76
QY      62 -----GRLAEVCTV 70
Db      77 APCGAAGPALSPVPVPHALALROAGDPSRRYRGDAEMSSOLHLPTTARGRFATVVEE 136
QY      71 LRLGITMGKVVSLYSVAAGLAVDCVROAPAMVHALVDCLGFEVFKTLATWLRRGGMT 130

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```

Db      137 LFRDGVNMGRIYAFEFEGGVMSESVNREMSPLVDNIALMTEYLNRHLHTWIDNGMD 196
QY      131 DVLKCV-VSTDGFRSHWL-VATLCS 154
Db      197 AFVELYGPMSRPLDFDSWLSLTKTLIS 222

```

## RESULT 12

```

AAG64038
ID      AAG64038 standard; protein; 239 AA.
XX
AC      AAG64038;
XX
DT      10-SEP-2001 (first entry)
XX
DE      Human Bcl-2 protein mutant #3.
XX
KW      Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
PN      WO200142459-A1.
XX
PD      14-JUN-2001.
XX
PF      07-DEC-2000; 2000MO-JP08667.
XX
PR      09-DEC-1999; 99JP-0350427.
XX
PA      (HISM ) HISAMITSU PHARM CO LTD.
XX
PI      Shlbazaki F, Kuma H;
XX
DR      WPI; 2001-381681/40.
XX
PT      New apoptosis inhibitors, useful for treating apoptosis related
XX      disorders -
XX
PS      Claim 7; Page 33-34; 43pp; Japanese.
XX
CC      The invention relates to an apoptosis inhibitor comprising the
CC      amino acid sequence of Bcl-2 protein in which at least one serine
CC      residue is substituted by alanine or aspartic acid. The protein has
CC      increased apoptosis inhibitory activity compared with the wild type
CC      Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment
CC      of disorders caused by apoptosis. The present sequence is a mutant
CC      Bcl-2 protein of the invention.
XX
SQ      Sequence 239 AA;

```

Query Match 14.9%; Score 131; DB 22; Length 239;

Best Local Similarity 19.4%; Pred. No. 9e-07;

Matches 40; Conservative 25; Mismatches 53; Indels 88; Gaps 4;

```

QY      37 EYVHARLLRAGLSM-----SAPERASAPAG----- 61
Db      17 KIHYKLSQRYGEMDAGVGAAPGGAAPAGIFSSQPGHTPHPAASRDVPARTSPLOTPA 76
QY      62 -----GRLAEVCTV 70
Db      77 APCGAAGPALSPVPVPHALALROAGDPSRRYRGDAEMSSOLHLPTTARGRFATVVEE 136
QY      71 LRLGITMGKVVSLYSVAAGLAVDCVROAPAMVHALVDCLGFEVFKTLATWLRRGGMT 130
Db      137 LFRDGVNMGRIYAFEFEGGVMSESVNREMSPLVDNIALMTEYLNRHLHTWIDNGMD 196
QY      131 DVLKCV-VSTDGFRSHWL-VATLCS 154
Db      197 AFVELYGPMSRPLDFDSWLSLTKTLIS 222

```

RESULT 13  
AAP80987  
ID AAP80987 standard; protein; 239 AA.  
XX  
AC AAP80987;  
XX  
DT 17-DEC-1990 (first entry)  
XX  
DE Sequence of bcl-2-alpha encoded by sequence of bcl-2 cDNA corresp. to  
DE the 5.5 kb transcript.  
XX  
KW B-cell neoplasm; diagnosis; follicular lymphomas.  
XX  
OS Homo sapiens.  
XX  
PN EP252685-A.  
XX  
PD 13-JAN-1988.  
XX  
PF 02-JUL-1987; 87EP-0305863.  
XX  
PR 09-JUL-1986; 86US-0883687.  
XX  
PA (WIST-) WISTAR CORP.  
XX  
PI Tsujimoto Y, Croce CM;  
XX  
DR WPI: 1988-008633/02.  
DR N-PSDB: AAN81292.  
XX  
XX  
PT Detection of B-cell neoplasms -  
PT by extn. of proteins or RNA from B-cells and quantitation using  
PT specific antibody or DNA probe  
XX  
PS Claim 12; Fig 2A-2D; 23pp; English.  
XX  
XX  
CC A human bcl-2 gene substantially free of introns is claimed. Also  
CC claimed is a substantially pure preparation of a protein having an  
CC N-terminal end encoded by the first exon of the human bcl-2 gene wherein  
CC said protein is bcl-2-alpha having about 239 (AAP80987) or 205 (AAP80988)  
CC AA residues. B-cell neoplasms which are associated with t(14;18)  
CC chromosome translocations cause an increase in expression of both the  
CC mRNA and the protein prods. of the bcl-2 gene. This is used to detect  
CC B-cell neoplasms including follicular lymphomas as well as other  
CC lymphomas. Bacterial isolates available as ATCC 67147 and 67148 can be  
CC used to express bcl-2 gene products alpha (AAN81292) and beta (AAN91293)  
CC resp. in bacteria.  
XX  
SQ Sequence 239 AA;  
Query Match 14.8%; Score 130; DB 9; Length 239;  
Best Local Similarity 19.4%; Pred. No. 1.2e-06;  
Matches 40; Conservative 25; Mismatches 53; Indels 88; Gaps 4;  
OY 37 EYVHRLRLRAGLSW-----SAPERASAPG----- 61  
DB 17 KYIHVRLSQRGEWDAGVGAAPGAPGIFSSQPGHTPPAASRDPVARTSPLQTPA 76  
OY 62 -----GRLAEVCTV 70  
DB 77 APGAAGALSPVPVPHALRQAGDDFSRRYRGDFAEMSSOLHTPTTARGRFATVVEE 136  
OY 71 LRLIGITMGKVVSLYSVAGIACVDCVROAQPAMVHALVDCIGEFVRKTLATLRRRGWT 130  
DB 137 LFRDGVNMGRIYAFEEFGVCMVESVNREMSPLVNIALMTETYLNRHLHTWIDQNGMD 196  
OY 131 DVLKCV-VSTDPGFRSHL-VATLCS 154  
DB 197 AFVELYGPSMRPLFDFSWLSIKTLIS 222

RESULT 14  
AAR42312  
ID AAR42312 standard; Protein; 239 AA.  
XX  
AC AAR42312;  
XX  
DT 03-MAY-1994 (first entry)  
XX  
DE Bcl-2 oncogene product.  
XX  
DE Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;  
DE expression; myc.  
XX  
KW Homo sapiens.  
XX  
OS WO9320200-A.  
XX  
PN 14-OCT-1993.  
XX  
PD 02-APR-1993; 93WO-GB00686.  
XX  
PF 02-APR-1992; 92GB-0007275.  
XX  
PR 02-APR-1992; 92GB-0007276.  
XX  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
XX  
PI Evan GI;  
XX  
DR WPI: 1993-336908/42.  
DR N-PSDB: AAO49815.  
XX  
XX  
PT Treating tumour cells by de-inhibiting Myc-induced apoptosis -  
PT esp. by inhibiting expression of the BCL-2 oncogene e.g. with  
PT antisense oligo:nucleotide(s), also increasing survival of  
PT cultured cells by expressing BCL-2  
XX  
PS Disclosure: Page 76-77; 109pp; English.  
XX  
XX  
CC A DNA construct comprising the bcl-2 coding sequence under control  
CC of elements allowing its expression is claimed. Myc-induced cell  
CC death can be inhibited in cultured cells by expressing bcl-2.  
CC Myc-induced cell death can be de-inhibited in tumour cells by admin.  
CC of bcl-2 antisense oligonucleotides.  
XX  
SQ Sequence 239 AA;  
Query Match 14.8%; Score 130; DB 14; Length 239;  
Best Local Similarity 19.4%; Pred. No. 1.2e-06;  
Matches 40; Conservative 25; Mismatches 53; Indels 88; Gaps 4;  
OY 37 EYVHRLRLRAGLSW-----SAPERASAPG----- 61  
DB 17 KYIHVRLSQRGEWDAGVGAAPGAPGIFSSQPGHTPPAASRDPVARTSPLQTPA 76  
OY 62 -----GRLAEVCTV 70  
DB 77 APGAAGALSPVPVPHALRQAGDDFSRRYRGDFAEMSSOLHTPTTARGRFATVVEE 136  
OY 71 LRLIGITMGKVVSLYSVAGIACVDCVROAQPAMVHALVDCIGEFVRKTLATLRRRGWT 130  
DB 137 LFRDGVNMGRIYAFEEFGVCMVESVNREMSPLVNIALMTETYLNRHLHTWIDQNGMD 196  
OY 131 DVLKCV-VSTDPGFRSHL-VATLCS 154  
DB 197 AFVELYGPSMRPLFDFSWLSIKTLIS 222

RESULT 15  
AAR70331  
ID AAR70331 standard; Protein; 239 AA.  
XX  
AC AAR70331;  
XX  
DT 27-SEP-1995 (first entry)  
XX



DE Human bcl-2 protein.  
 XX Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;  
 KM chemoresistance.  
 XX

OS Homo sapiens.

PN WO9508350-A.

PD 30-MAR-1995.

PF 20-SEP-1994; 94WO-US10725.

PR 20-SEP-1993; 93US-0124256.

PA (REED/) REED J C.

PI Reed JC;

DR WPI; 1995-139394/18.

XX Anticodon oligomers which bind to bcl-2 mRNA - for the treatment  
 PT of human solid tumours, esp. breast cancer  
 XX

PS Disclosure; Page 71-72; 108pp; English.

XX The human bcl-2 gene encodes a 25 kDa protein (AAR70331). Antisense  
 CC oligonucleotides have been designed to bind sites in mRNA transcribed  
 CC from the bcl-2 gene, thereby reducing expression of the bcl-2 protein  
 CC and inducing cell death in certain cancer cells.  
 XX

SQ Sequence 239 AA;

Query Match 14.8%; Score 130; DB 16; Length 239;

Best Local Similarity 19.4%; Pred. No. 1.2e-06;  
 Matches 40; Conservative 25; Mismatches 53; Indels 88; Gaps 4;

OY 37 EYVHARLLRAGLSW-----SAPERASPAAG----- 61

DB 17 KYTHYKLSQSGYEMDAGDVCAAPGAPAPAGIRSSQGHTPHPASRDVPARTSPLOTPTA 76

OY 62 -----GRLAEYCTV 70

DB 77 APGAAGPALSPVPVPHALALRQAGDPSRRYRGDFEAMSSQLHLTPFTARGRFATVEE 136

OY 71 LRLGITWGKVSGLYSAAGLAVDCYRQAPAWVHALVDCLGFEVRRKTLATWLRRGWT 130

DB 137 LFRDGVNMGRIYAFEEGGVMCYESVNRKMSPLVDNIALMTEYLNRHLHTWTIQDNGWD 196

OY 131 DVLKCV-VSTDPGFRSHWL-VATLCS 154

DB 197 AFVELYGPMSWRPLDFPSWLSLKTLLS 222

Search completed: April 29, 2003, 11:23:22  
 Job time : 26.9661 secs



GenCore version 5.1.4-p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2003, 11:19:46 ; Search time 27.2507 Seconds  
(without alignments)  
1610.532 Million cell updates/sec

Title: US-09-682-667-6  
Perfect score: 1100  
Sequence: 1 MEVLRRSSVFAAEIMDAFDR.....TLCSPGRFLKAFLLPER 213

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_21:\*  
1: sp-archaea:\*  
2: sp-bacteria:\*  
3: sp-fungi:\*  
4: sp-human:\*  
5: sp-invertebrate:\*  
6: sp-mammal:\*  
7: sp-mhc:\*  
8: sp-organelle:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-rodent:\*  
12: sp-virus:\*  
13: sp-vertebrate:\*  
14: sp-unclassified:\*  
15: sp-virus:\*  
16: sp-bacteriap:\*  
17: sp-archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1100	100.0	213	4 Q9UL32	Q9UL32 homo sapien
2	1076	97.8	213	11 Q35425	Q35425 rattus norv
3	1017.5	92.5	212	4 Q9UMX3	Q9UMX3 homo sapien
4	874	79.5	213	13 Q91812	Q91812 gallus gall
5	868	78.9	213	13 Q9DGS5	Q9DGS5 gallus gall
6	828.5	75.3	170	11 Q88857	Q88857 rattus norv
7	240.5	21.9	300	5 Q9V9C8	Q9V9C8 drosophila
8	238.5	21.7	299	5 Q8T8Y5	Q8T8Y5 drosophila
9	238.5	21.7	313	5 Q9NGX3	Q9NGX3 drosophila
10	230	20.9	247	5 Q9V612	Q9V612 drosophila
11	209.5	19.0	317	5 Q95U83	Q95U83 drosophila
12	158	14.4	236	11 Q923R6	Q923R6 cricetus
13	155	14.1	235	11 Q35843	Q35843 mus musculu
14	154	14.0	233	11 Q35844	Q35844 mus musculu
15	150.5	13.7	188	11 Q9QWX2	Q9QWX2 mus musculu
16	149	13.5	233	6 Q8SQ42	Q8SQ42 felis silve

17	147.5	13.4	233	6 Q9MZS7	Q9MZS7 ovis aries
18	147.5	13.4	233	6 Q9NIA2	Q9NIA2 sus scrofa
19	146.5	13.3	188	4 Q9H1R6	Q9H1R6 homo sapien
20	146.5	13.3	219	11 Q99N36	Q99N36 mus musculu
21	145.5	13.2	179	4 Q9NNG7	Q9NNG7 homo sapien
22	145.5	13.2	192	13 Q919M4	Q919M4 brachydanto
23	145	13.0	238	13 Q90Z98	Q90Z98 brachydanto
24	142.5	13.0	233	6 Q9MYW4	Q9MYW4 cryotolagus
25	142	12.9	217	11 Q99N35	Q99N35 mus musculu
26	138.5	12.6	204	13 Q90Z82	Q90Z82 xenopus lae
27	137.5	12.5	173	4 Q8W249	Q8W249 homo sapien
28	137.5	12.5	180	6 Q9BDD5	Q9BDD5 bos taurus
29	136	12.4	163	6 Q9MZS6	Q9MZS6 ovis aries
30	136	12.4	221	13 Q98U13	Q98U13 xenopus lae
31	135.5	12.3	180	6 Q9BDX7	Q9BDX7 bos taurus
32	134.5	12.2	193	11 Q88996	Q88996 rattus norv
33	132.5	12.0	178	11 Q9CYW5	Q9CYW5 mus musculu
34	131.5	12.0	149	6 Q9GMG7	Q9GMG7 ovis aries
35	131.5	12.0	192	6 Q8SQ43	Q8SQ43 felis silve
36	126.5	11.5	209	11 Q9JKS9	Q9JKS9 rattus norv
37	126.5	11.5	330	11 Q921P3	Q921P3 rattus norv
38	126	11.5	331	11 P97287	P97287 mus musculu
39	124	11.3	173	11 Q9JKL3	Q9JKL3 rattus norv
40	116	10.5	211	13 Q9W6F1	Q9W6F1 gallus gall
41	116	10.5	350	4 Q9QNUJ	Q9QNUJ homo sapien
42	110.5	10.0	114	4 Q9NR76	Q9NR76 homo sapien
43	104.5	9.5	172	11 Q55177	Q55177 mus musculu
44	101	9.2	172	11 Q55179	Q55179 mus musculu
45	97.5	8.9	89	13 Q8UWJ1	Q8UWJ1 gallus gall

## ALIGNMENTS

RESULT 1	Q9UL32	PRELIMINARY:	PRT:	213 AA.
AC	Q9UL32:			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Bcl-2 related ovarian killer.			
GN	BOX.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Hsu S.Y., Hsueh A.J.W.;			
RT	*cDNA cloning of the human Bcl gene.*;			
RL	Submitted (SEP-1998) to the EMBL/GenBank/DDBI databases.			
DR	EMBL; AF089746; AAF09129.1; -			
DR	InterPro; IPR000712; Bcl2_BH.			
DR	InterPro; IPR002475; Bcl2_family.			
DR	Pfam; PF00452; Bcl-2; 1.			
DR	SMART; SM00337; BCL; 1.			
DR	PROSITE; P550062; BCL2_FAMILY; 1.			
DR	PROSITE; 213 AA; 23540 MW; 59509F8C730517F CRC64;			
DR	SEQUENCE			
QY	Query Match	100.0%;	Score 1100;	DB 4; Length 213;
QY	Best local similarity	100.0%;	Pred. No. 7.1e-89;	
QY	Matches 213;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
DB	1 MEVLRRSSVFAAEIMDAFDRPPTDKELVAQAKLGRYYHARLLRGLSKSAPERRSPAP 60			
QY	1 MEVLRRSSVFAAEIMDAFDRPPTDKELVAQAKLGRYYHARLLRGLSKSAPERRSPAP 60			
DB	1 MEVLRRSSVFAAEIMDAFDRPPTDKELVAQAKLGRYYHARLLRGLSKSAPERRSPAP 60			
QY	61 GGLAEVCYVLLRGLLEQIRPSVYRNVAAROLHIFLOSPPVTDALFVAGHIFSGIT 120			
DB	61 GGLAEVCYVLLRGLLEQIRPSVYRNVAAROLHIFLOSPPVTDALFVAGHIFSGIT 120			
QY	121 GGRVSLSYSAAGLAVDCAVROAPAMVHALVDCLGFEVRKTLATWLRNRGGMTDLKCVV 180			

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DB 121 WGVVSLVSAAGLAVDCVROAPAMVHALVDCLEFVAKTLATWLRGGMTDVLKCV 180
OY 181 STKPGFRSHMWLVATLCSFGRLKAAFFLLP 213
DB 181 STKPGFRSHMWLVATLCSFGRLKAAFFLLP 213

```

## RESULT 2

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035425 PRELIMINARY: PRT: 213 AA.

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ID 035425
AC 035425.
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE BCL-2-related ovarian killer protein.
GN BOK OR BOKL OR BOK OR MTD.
OS Rattus norvegicus (Rat), and
Mus musculus (Mouse), Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116, 10090;
[1]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY, TESTIS, AND UTERUS;
RX MEDLINE=96024143; Pubmed=9356461;
RA Hsu S.Y., Kaipia A., Mccree E., Lomeli M., Hsueh A.J.W.;
RT "Bok is a pro-apoptotic BCL-2 protein with restricted expression in
reproductive tissues and heterodimerizes with selective anti-apoptotic
BCL-2 family members."
RT Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).
[2]
RN SEQUENCE FROM N.A.
RP SPECIES-Rat; STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY, TESTIS, AND UTERUS;
RC SPECIES-Rat; STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY, TESTIS, AND UTERUS;
RA Hsu S.Y., Hsueh A.J.W.;
RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP SPECIES-Mouse;
RA Inohara N., Ekheraie D., Garcia I., Carrilo R., Merino J., Merry A.,
Chen S., Nunez G.;
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
RX EMBL: AF027954; AAB87418.1; -
DR EMBL: AF027707; AAC53582.1; -
DR MGI: 1858494; BOK.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF00452; BCL-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
SO SEQUENCE 213 AA; 23456 MW; F8755C45CB05D626 CRC64;

```

```

Query Match 97.8%; Score 1076; DB 11; Length 213;
Best Local Similarity 98.6%; Pred. No. 9.1e-87;
Matches 210; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

OY 1 MEVLRSSVFAAEIMDARDRPTDKELVAQAALGREYVHARLLRAGLSWSPERASAP 60
DB 1 MEVLRSSVFAAEIMDARDRPTDKELVAQAALGREYVHARLLRAGLSWSPERASAP 60
OY 61 GRLAEVCTVLLRLGDELLEQIRPSYRVNARQLHIPLOSEPVYDAFLAVAGHIFSAGIT 120
DB 61 GRLAEVCTVLLRLGDELLEQIRPSYRVNARQLHIPLOSEPVYDAFLAVAGHIFSAGIT 120
OY 121 WGVVSLVSAAGLAVDCVROAPAMVHALVDCLEFVAKTLATWLRGGMTDVLKCV 180
DB 121 WGVVSLVSAAGLAVDCVROAPAMVHALVDCLEFVAKTLATWLRGGMTDVLKCV 180
OY 181 STKPGFRSHMWLVATLCSFGRLKAAFFLLP 213
DB 181 STKPGFRSHMWLVATLCSFGRLKAAFFLLP 213

```

## RESULT 3

```

09UMX3 PRELIMINARY: PRT: 212 AA.

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```

ID 09UMX3
AC 09UMX3.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE BCL-2-related ovarian killer protein (Similar to BCL-2-related ovarian
killer protein-like-PENDING) (BCL-2-related ovarian killer
protein-like).
GN BOK.
OS Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA Zhang H.;
RT "Gene expression of a human homolog of BCL-2-related ovarian killer
protein."
RT Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC TISSUE-MUSCLE;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RC TISSUE-MUSCLE;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF174487; AAD51719.1; -
DR EMBL: BC006203; AAH06203.1; -
DR EMBL: BC017214; AAH17214.1; -
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF00452; BCL-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
SO SEQUENCE 212 AA; 23280 MW; 053ED605F8EF5B2 CRC64;

```

```

Query Match 92.5%; Score 1017.5; DB 4; Length 212;
Best Local Similarity 93.9%; Pred. No. 1.2e-81;
Matches 200; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

```

```

OY 1 MEVLRSSVFAAEIMDARDRPTDKELVAQAALGREYVHARLLRAGLSWSPERASAP 60
DB 1 MEVLRSSVFAAEIMDARDRPTDKELVAQAALGREYVHARLLRAGLSWSPERASAP 60
OY 61 GRLAEVCTVLLRLGDELLEQIRPSYRVNARQLHIPLOSEPVYDAFLAVAGHIFSAGIT 120
DB 61 GRLAEVCTVLLRLGDELLEQIRPSYRVNARQLHIPLOSEPVYDAFLAVAGHIFSAGIT 119
OY 121 WGVVSLVSAAGLAVDCVROAPAMVHALVDCLEFVAKTLATWLRGGMTDVLKCV 180
DB 121 WGVVSLVSAAGLAVDCVROAPAMVHALVDCLEFVAKTLATWLRGGMTDVLKCV 179
OY 181 STKPGFRSHMWLVATLCSFGRLKAAFFLLP 213
DB 181 STKPGFRSHMWLVATLCSFGRLKAAFFLLP 212

```

## RESULT 4

```

091812 PRELIMINARY: PRT: 213 AA.

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```

ID 091812
AC 091812.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE BCL-2-related ovarian killer protein.
OS Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

```

OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20487164; PubMed=11034351;  
 RA Zhang H., Holzgrevé W., De Geyter C.;  
 RT "Evolutionarily conserved Bcl proteins in the Bcl-2 family.";  
 RL FEBS Lett. 480:311-313(2000).  
 DR EMBL: AF275944; AAF81282.1; -  
 DR InterPro: IPR000712; Bcl2-BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 SO SEQUENCE 213 AA; 23619 MW; B3AF7049F25442E3 CRC64;

Query Match 79.5%; Score 874; DB 13; Length 213;  
 Best Local Similarity 77.0%; Pred. No. 4.9e-69;  
 Matches 164; Conservative 22; Mismatches 27; Indels 0; Gaps 0;

OY 1 MEVLRRSSVFAAEIMDAFDRMPTDKELVAQAAGREYVHARLLRAGLSMSAPERASAP 60  
 DB 1 MEVLRRSSVFAAEVMEYFDRSPDKELVSOAKALCRDIINSRLIRAGVSMKPEHNPVP 60  
 OX [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98024143; PubMed=9356461;  
 RA Hsu S.Y., Kaipia A., McGee E., Lomeli M., Hsueh A.J.W.;  
 RT "Bcl-2 is a pro-apoptotic bcl-2 protein with restricted expression in  
 reproductive tissues and heterodimerizes with selective anti-apoptotic  
 bcl-2 family members.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).  
 DR EMBL: AF051093; AAC61928.1; -  
 DR InterPro: IPR000712; Bcl2-BH.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 SO SEQUENCE 170 AA; 18729 MW; 15E54361F448CF16 CRC64;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20487164; PubMed=11034351;  
 RA Zhang H., Holzgrevé W., De Geyter C.;  
 RT "Evolutionarily conserved Bcl proteins in the Bcl-2 family.";  
 RL FEBS Lett. 480:311-313(2000).  
 DR EMBL: AF275944; AAF81282.1; -  
 DR InterPro: IPR000712; Bcl2-BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 SO SEQUENCE 213 AA; 23619 MW; B3AF7049F25442E3 CRC64;

Query Match 78.9%; Score 868; DB 13; Length 213;  
 Best Local Similarity 76.1%; Pred. No. 1.7e-68;  
 Matches 162; Conservative 23; Mismatches 28; Indels 0; Gaps 0;

OY 1 MEVLRRSSVFAAEIMDAFDRMPTDKELVAQAAGREYVHARLLRAGLSMSAPERASAP 60  
 DB 1 MEVLRRSSVFAAEVMEYFDRSPDKELVSOAKALCRDIINSRLIRAGVSMKPEHNPVP 60  
 OX [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20487164; PubMed=11034351;  
 RA Zhang H., Holzgrevé W., De Geyter C.;  
 RT "Evolutionarily conserved Bcl proteins in the Bcl-2 family.";  
 RL FEBS Lett. 480:311-313(2000).  
 DR EMBL: AF275944; AAF81282.1; -  
 DR InterPro: IPR000712; Bcl2-BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 SO SEQUENCE 213 AA; 23619 MW; B3AF7049F25442E3 CRC64;

DB 61 GKLAEVSAIILRLGDELEYIRPNVYRNRIAROLNISLHSEVYVDAFLAVALAAGIFTAGIT 120  
 OY 121 WGVVSLYSAAAGLAVDCVQAOPAMVHALVDCGFEVRKTLATWLRRGWTDVLCVY 180  
 DB 121 WGVVSLYSAAAGLAVDCVQAOPAMVHALVDCGFEVRKTLATWLRRGWTDVLCVY 180  
 OX [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98024143; PubMed=9356461;  
 RA Hsu S.Y., Kaipia A., McGee E., Lomeli M., Hsueh A.J.W.;  
 RT "Bcl-2 is a pro-apoptotic bcl-2 protein with restricted expression in  
 reproductive tissues and heterodimerizes with selective anti-apoptotic  
 bcl-2 family members.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).  
 DR EMBL: AF051093; AAC61928.1; -  
 DR InterPro: IPR000712; Bcl2-BH.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 SO SEQUENCE 170 AA; 18729 MW; 15E54361F448CF16 CRC64;

Query Match 75.3%; Score 828.5; DB 11; Length 170;  
 Best Local Similarity 74.4%; Pred. No. 3.7e-65;  
 Matches 167; Conservative 0; Mismatches 3; Indels 43; Gaps 1;

OY 1 MEVLRRSSVFAAEIMDAFDRMPTDKELVAQAAGREYVHARLLRAGLSMSAPERASAP 60  
 DB 1 MEVLRRSSVFAAEVMEYFDRSPDKELVSOAKALCRDIINSRLIRAGVSMKPEHNPVP 60  
 OX [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98024143; PubMed=9356461;  
 RA Hsu S.Y., Kaipia A., McGee E., Lomeli M., Hsueh A.J.W.;  
 RT "Bcl-2 is a pro-apoptotic bcl-2 protein with restricted expression in  
 reproductive tissues and heterodimerizes with selective anti-apoptotic  
 bcl-2 family members.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).  
 DR EMBL: AF051093; AAC61928.1; -  
 DR InterPro: IPR000712; Bcl2-BH.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 SO SEQUENCE 170 AA; 18729 MW; 15E54361F448CF16 CRC64;

AC 09Y9C8: 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)  
 DE Death EXECUTIONER Bcl-2 homolog protein (PROAPOPTOTIC BCL-2 homolog  
 DE DEBCL) (BCL-2 family member protein) (BCL-2 ORTHOLOG DBORG-1).  
 GN DEBCL OR DBORG1 OR BOK OR BCL2 OR ROB-1 OR CG12397.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=EMBryo;  
 RX MEDLINE=20105529; PubMed=2015529;  
 RA Igaki T., Kanuka H., Inohara N., Sawamoto K., Nunez G., Okano H.,  
 RA Miura M.;  
 RT "Drob-1, a Drosophila member of the Bcl-2/CED-9 family that promotes  
 RT cell death."; Proc. Natl. Acad. Sci. U.S.A. 97:662-667(2000).  
 RL [2]  
 RN REVISIONS TO N-TERMINUS.  
 RP Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20153510; PubMed=10684252;  
 RA Colussi P.A., Quinn L.M., Huang D.C.S., Coombe M., Read S.H.,  
 RA Richardson H., Kumar S.;  
 RT "Debcl, a proapoptotic Bcl-2 homologue, is a component of the  
 RT Drosophila melanogaster cell death machinery."; Cell Biol. 148:703-714(2000).  
 RL [4]  
 RN SEQUENCE FROM N.A.  
 RP Zhang H., Huang Q., Ke N., Matsuyama S., Hammock B., Godzik A.,  
 RA Reed J.C.;  
 RT "Drosophila pro-apoptotic Bcl-2/Bax homolog reveals evolutionary  
 RT conservation of cell death mechanisms."; J. Biol. Chem. 278:40040-40046(2003).  
 RL [5]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abiri J.F., Aghayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Berns P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burks K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K.C., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Dutilleul K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,  
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman I.J., Hernandez J.R., Houck J.,  
 RA Hosteln D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,  
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacile J.M.,  
 RA Palazzolo M., Peltzman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheller F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao G., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).  
 RL [6]  
 RN SEQUENCE FROM N.A.  
 RP Kurada P., White K.;  
 RT "Putative Drosophila homolog of mammalian Bcl-2-related ovarian killer  
 RT protein."; Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Zhou L., Steller H.;  
 RT "Potential Drosophila homologue of Bcl-2-related ovarian killer  
 RT (BOK)."; Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.  
 RL [8]  
 RN SEQUENCE FROM N.A.  
 RP Brachmann C.B., Jassim O.W., Wachsmuth B.D., Cagan R.L.;  
 RT "Dorg-1, a Drosophila Bcl-2 family member that functions in the  
 RT apoptotic response to UV-irradiation."; Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 RL EMBL; AB032430; BAA89603.2; -  
 DR EMBL; AF149798; AAF26841.1; ALT\_INIT.  
 DR EMBL; AF178430; AAF26289.1; -  
 DR EMBL; AF228044; AAF89165.1; -  
 DR EMBL; AE003789; AAF57365.1; ALT\_TERM.  
 DR EMBL; AF222004; AAF4324.1; -  
 DR EMBL; AF216752; AAF25955.1; ALT\_TERM.  
 DR EMBL; AF244352; AAF44714.1; -  
 DR FLYbase; Fpgn0029131; debcl.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR InterPro; IPR000822; Znf\_C2H2.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PSS0062; BCL2\_FAMILY; 1.  
 DR PROSITE; PSS0157; ZINC\_FINGER\_C2H2\_2; 4.  
 KW DNA-binding; Zinc-finger.  
 FT CONFLICT 1 86 MISSING (IN REF. 4).  
 FT CONFLICT 215 215 I -> V (IN REF. 1).  
 FT CONFLICT 217 217 C -> R (IN REF. 4).  
 SQ SEQUENCE 300 AA: 32940 MW: 42290 ADC3D0942 CRC64;  
 Query Match 21.9%; Score 240.5; DB 5; Length 300;  
 Best Local Similarity 35.3%; Pred. No. 3,1e-13;  
 Matches 55; Conservative 27; Mismatches 65; Indels 9; Gaps 4;  
 QY 26 ELVAQKALGRYVARILRLA-TSMASPER-----ASPARGLAEVCVILRLGDEEO 80  
 DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 155  
 QY 96 DITNGKCGCGYIRRLRAGVLRNKKYQRLRNILDPSSHVVEVPALMSKEELER 155  
 DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 156  
 QY 81 IPPSVRYNAROL-HIP---LQSEPVYTDALFVAGHIFSAITGKKVSLTSAAGLAV 136  
 DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 136  
 QY 156 MPRVYTNISRLSRPFELDESDMAPRLNLVAKDLFRSSITGKIISTITAVCGGPAI 215  
 DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 215  
 QY 137 DCVQAQAPAMVHALVDCGCEFYKRLATWLRRRGGW 172  
 DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 172  
 QY 216 DCVROGHFDYDLOCLLDGLAEIIEDLVYLWINDGWM 251  
 DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 251  
 RESULT 8  
 Q8T8Y5 PRELIMINARY: PRT: 299 AA. ;  
 AC Q8T8Y5;  
 DT 01-JUN-2002 (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)

DE AT16536p.  
 GN BUFEY.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Chape M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nanco J., Pacleb J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celinker S.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY075219; AAL6086.1; -  
 SQ SEQUENCE 299 AA; 33379 MW; 7FB125A6B7323B23 CRC64;

Query Match 21.7%; Score 238.5; DB 5; Length 299;  
 Best Local Similarity 31.1%; Pred. No. 4.6e-13;  
 Matches 66; Conservative 33; Mismatches 82; Indels 31; Gaps 8;

OY 25 KELVAQKALGREYVHARLRAGL--SWSAPERASPAFG---GRAEVCVTLRLGDEL 78  
 DB 87 QDIISQRCICGHIKRLRRSLGFNNKILQIRISITSGTSMGIYADVPAVQVLDL 146  
 OY 79 EOIRPSVYRNVAROL-----HIPLOSEPVTDAFLAVAGHIFSGITWGVSLYSA 130  
 DB 147 ERHMPRTYNGVAROICRNPGGEHTP---DAVSLIGAAGRELFRVELTWISVLSLFAI 202  
 OY 131 AGLAVDCVROAPAMVHALVDLIGFVRKTLATWLRRRGW---TDVLKCVSTRKPGF 186  
 DB 203 AGLAVDCVROAGREYLPKLMESVSEIYDELPWLNENGSWGINTHVLPTNSLNP-- 260  
 OY 187 RSHWLAVTL-CSPG-----RFLKAFFLLPE 212  
 DB 261 -LEMTTLVIGVFPGLILVEMILRFENLIVPK 291

## RESULT 9

O9NGX3 PRELIMINARY; PRT; 313 AA.  
 ID O9NGX3;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Bcl-2-like protein BUFEY (Fragment).  
 GN BUFEY OR CG6238.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=20153510; PubMed=10684252;  
 RA Colussi P.A., Quin L.M., Huang D.C., Coombe M., Read S.H.,  
 RA Richardson H., Kumar S.;  
 RT \*Debel, a proapoptotic bcl-2 homologue, is a component of the  
 RT Drosophila melanogaster cell death machinery.";  
 RL J. Cell Biol. 148:703-714(2000).  
 DR EMBL: AF237864; AAF44120.1; -  
 DR HSSP: 007817; 1MAZ.  
 DR FlyBase: FBgn0040491; BUFEY.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PSS0062; BCL2\_FAMILY; 1.  
 FT NON TER 1  
 SO SEQUENCE 313 AA; 34909 MW; 775A41FDD5B678E CRC64;

Query Match 21.7%; Score 238.5; DB 5; Length 313;  
 Best Local Similarity 31.1%; Pred. No. 4.8e-13;  
 Matches 66; Conservative 33; Mismatches 82; Indels 31; Gaps 8;

OY 25 KELVAQKALGREYVHARLRAGL--SWSAPERASPAFG---GRAEVCVTLRLGDEL 78  
 DB 101 QDIISQRCICGHIKRLRRSLGFNNKILQIRISITSGTSMGIYADVPAVQVLDL 160  
 OY 79 EOIRPSVYRNVAROL-----HIPLOSEPVTDAFLAVAGHIFSGITWGVSLYSA 130  
 DB 161 ERHMPRTYNGVAROICRNPGGEHTP---DAVSLIGAAGRELFRVELTWISVLSLFAI 216  
 OY 131 AGLAVDCVROAPAMVHALVDLIGFVRKTLATWLRRRGW---TDVLKCVSTRKPGF 186  
 DB 217 AGLAVDCVROAGREYLPKLMESVSEIYDELPWLNENGSWGINTHVLPTNSLNP-- 274  
 OY 187 RSHWLAVTL-CSPG-----RFLKAFFLLPE 212  
 DB 275 -LEMTTLVIGVFPGLILVEMILRFENLIVPK 305

## RESULT 10

O9V612 PRELIMINARY; PRT; 247 AA.

ID O9V612;  
 AC O9V612;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE CG8238 protein.  
 GN BUFEY OR CG8238.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Kelchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svitek S., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wastaman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*."  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003825; AAF58628.1;  
 DR HSSP: Q07817; 1MA2  
 DR FlyBase: FBgn0040491; Buffy.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL2\_FAMILY.  
 DR PROSITE: PS50062; BCL2\_FAMILY.  
 SO SEQUENCE 247 AA; 27466 MW; A2C4325AF4C1620 CRC64;

Query Match 20.9%; Score 230; DB 5; Length 247;  
 Best Local Similarity 33.3%; Pred. No. 2e-12;  
 Matches 54; Conservative 28; Mismatches 62; Indels 18; Gaps 4;

OY 25 KEIVAAQAKALGREYVHARLRAGL--SNSAPRASPARG---GRLAECYVLLRLGDEL 78  
 DB 87 ODIISGRCICGHYIKRRLRSGLFNKILGLQIRISILGSTMGIVRDVFPAYQVYLGDEL 146  
 OY 79 EDIRSVRNVAROL-----HIPLOSEPVYTDAPLAVAGHIFSAGITGKVSLSYA 130  
 DB 147 ERMHRIITNGVARQICRNPGGEFHP-----DAVSLLGAVGELREVELTMSKVSLSFAI 202  
 OY 131 AAGLAVDCVRAQAPAMVHALVDCLEFVRKLTATWLRKRGW 172  
 DB 203 AGGLSVDCVRQGHPEYLPRLMESVSEVIEDELVPMINENGW 244

RESULT 11  
 ID 095083 PRELIMINARY; PRT; 317 AA.  
 AC 095083;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE GH01265P.  
 GN DEBCL OR CG12397.  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydriidae; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Flise E., George R.,  
 RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.,  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY058249; AAL13478.1;  
 DR FlyBase: FBgn0029131; debcl.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 SO SEQUENCE 317 AA; 34649 MW; 46B22FED1CC6F01F CRC64;

Query Match 19.0%; Score 209.5; DB 5; Length 317;  
 Best Local Similarity 34.4%; Pred. No. 1.7e-10;  
 Matches 54; Conservative 28; Mismatches 64; Indels 11; Gaps 5;

OY 26 ELVAAKALGREYVHARLRAG-LSMSAPR-----ASPARGRLAEVGVLLRLGDEL 80  
 DB 96 DIINGKCLCGGYIRARLRRAKRYQRLRLNLDPESSHVVEVPALMSKEELER 155  
 OY 81 IRPSVYRNVAROL-HIP--LQSEPVYTDAPLAVAGHIFSAGITGKVSLSYAAGLAV 136  
 DB 136 MHPRYVTINSLRSLRAPGCELESDMAPMLNLVAKDLFRSSITGKTIISITAVCGGFAI 215

OY 137 DCVROAQPAMVHALVDCLEFVRK--TLATWLRRCG 171  
 DB 216 DCVROGHEDYDCLIDGLAEIIGRGLLADRQRWVG 252

RESULT 12  
 ID 092386 PRELIMINARY; PRT; 236 AA.  
 AC 092386;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE B-cell lymphoma protein 2.  
 GN BCL2.  
 OS *Cricetus longicaudatus* (Long-tailed hamster) (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 CC *Cricetus*.  
 OX NCBI\_TaxID=10030;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Lai D.Z., Chen W., Wang H.T.,  
 RT "Construction of a robust CHO cell line for biopharmaceutical use."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF043339; AAK92201.1;  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH.  
 DR InterPro: IPR002475; Bcl2\_FAMILY.  
 DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; UNKNOWN.1.  
 DR PROSITE: PS01258; BH2; UNKNOWN.1.  
 DR PROSITE: PS01259; BH3; UNKNOWN.1.  
 DR PROSITE: PS01260; BH4.1; UNKNOWN.1.  
 DR PROSITE: PS50063; BH4.2; 1.  
 SO SEQUENCE 236 AA; 26500 MW; BEDF052EF32CA888 CRC64;

Query Match 14.4%; Score 158; DB 11; Length 236;  
 Best Local Similarity 21.8%; Pred. No. 4e-06;  
 Matches 47; Conservative 36; Mismatches 77; Indels 56; Gaps 7;

OY 28 VAQAKALG-----REYVHARLRAGLSW-----SAPERASPARG----- 61  
 DB 1 MAQAGRTGYDNREIYMKYIHYKLSORGVEWDVADAPLGAAPPGIFSPQESNPYPA 60  
 OY 62 -----GRLAECYVLLRLGDELEQIRSVYRNVAR-----OLHT-P 96  
 DB 61 VHRDMAARTSPLRPIVATGTPTLSPVPVYHLTLRRAGDDFSRRYRDPAEKSSQLHLTP 120  
 OY 97 LQSEPVYTDAPLAVAGHIFSAGITGKVSLSYAAGLAVDCVROAQPAMVHALVDCLE 156  
 DB 121 FTAR-----GRFATVVEELFRDGVNMGRIVAFPEEGVACVESVNRKMSPLVDNLAWMTE 176  
 OY 157 FVRKLTATWLRKRGWTDVLCV-VSTRKGFGRSHWL 191  
 DB 177 YLNRHLTHWIDONGMDAFVELYGPSVRPLDFESWL 212

RESULT 13  
 ID 035843 PRELIMINARY; PRT; 235 AA.  
 AC 035843;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Bcl-2-gamma.  
 GN BCL2L.  
 OS *Mus musculus* (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.







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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:18:26 ; Search time 7.50783 Seconds

(without alignments)  
1176.699 Million cell updates/sec

Title: US-09-682-667-6  
Perfect score: 1100  
Sequence: 1 MEVLRRSSVFSAEIMDAFDR.....TLCSEGRFLKAFFLLPER 213

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 10%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	167.5	15.2	236	1	BCL2_RAT
2	164.5	13.0	229	1	BCL2_BOVIN
3	159.5	14.5	236	1	BCL2_CRITO
4	157.5	14.3	236	1	BCL2_MOUSE
5	155	14.1	228	1	ARL_XENLA
6	155	14.1	233	1	BCL2_CHICK
7	153.5	14.0	239	1	BCL2_HUMAN
8	150.5	13.7	233	1	BCLX_MOUSE
9	150.5	13.7	233	1	BCLX_RAT
10	148.5	13.5	218	1	BAXB_HUMAN
11	146.5	13.3	233	1	BCLX_HUMAN
12	146.5	13.3	233	1	BCLX_PIG
13	143.5	13.0	192	1	BAXA_HUMAN
14	138.5	12.6	204	1	ARL1_XENLA
15	137.5	12.5	229	1	BCLX_CHICK
16	134.5	12.2	193	1	BCLX_MOUSE
17	133.5	12.1	192	1	BAXA_BOVIN
18	130.5	11.9	193	1	BCLW_HUMAN
19	129.5	11.8	192	1	BAXA_MOUSE
20	129.5	11.8	192	1	BAXA_RAT
21	128	11.6	208	1	BAK_MOUSE
22	127.5	11.6	211	1	BAK_HUMAN
23	127.5	11.6	211	1	BAK2_HUMAN
24	122.5	11.1	23	1	MCL1_HUMAN
25	116	10.5	350	1	BAID_HUMAN
26	110.5	10.0	143	1	CARB_HUMAN
27	97.5	8.9	115	1	CARB_MYCTU
28	95.5	8.7	172	1	BFL1_MOUSE
29	91.5	8.3	175	1	BFL1_HUMAN
30	88.5	8.0	1121	1	CARB_MYCTE
31	85.5	7.8	2003	1	NTC4_HUMAN
32	85	7.7	551	1	SMA4_MOUSE
33	85	7.7	552	1	SMA4_HUMAN
	85	7.7	552	1	SMA4_PIG
					Q9gkq9 sus scrofa

34	85	7.7	552	1	SMA4_RAT	O70437 rattus norv
35	84	7.6	941	1	DNAB_RHOMR	O30477 rhodothermu
36	83	7.5	177	1	NR13_COTJA	O90343 coturnicu co
37	82.5	7.5	535	1	SSDH_HUMAN	P51649 homo sapien
38	82.5	7.5	1081	1	CARB_STNT3	Q55756 synchocyst
39	80.5	7.3	319	1	MOCB_STNP7	Q56208 synchococc
40	80.5	7.3	372	1	GDF1_HUMAN	P27539 homo sapien
41	80.5	7.3	385	1	RURE_PSEOL	P17052 pseudomonas
42	79.5	7.2	406	1	WCAL_SALRY	P26388 salmoneella
43	79.5	7.2	672	1	ACSA_PHYBL	O01576 phycomyces
44	78.5	7.1	1075	1	CNRA_ALCEU	P37972 alcailligenes
45	77	7.0	205	1	GTS1_ASCSU	P46436 ascaris suu

## ALIGNMENTS

RESULT 1	ID	STANDARD:	PRT:	236 AA.
BCL2_RAT	AC	P49950: 062837: 064032:		
BCL2_RAT	DT	01-OCT-1996 (Rel. 34, Created)		
BCL2_RAT	DT	01-NOV-1997 (Rel. 35, Last sequence update)		
BCL2_RAT	DT	15-JUN-2002 (Rel. 41, Last annotation update)		
BCL2_RAT	DE	Apoptosis regulator Bcl-2.		
BCL2_RAT	GN	BCL2 OR BCL-2.		
BCL2_RAT	OS	Rattus norvegicus (Rat).		
BCL2_RAT	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
BCL2_RAT	OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
BCL2_RAT	NCBI_TaxID	10116;		
BCL2_RAT	NP	SEQUENCE FROM N.A.		
BCL2_RAT	RC	TISSUE=Brain;		
BCL2_RAT	RA	MEDLINE=94193015; PubMed=8144041;		
BCL2_RAT	RT	Sato T., Irie S., Krajewski S., Reed J.C.;		
BCL2_RAT	RT	"Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";		
BCL2_RAT	RT	Gene 140:291-292(1994).		
BCL2_RAT	RT	[2]		
BCL2_RAT	NP	SEQUENCE FROM N.A.		
BCL2_RAT	RC	STRAIN=Sprague-Dawley; TISSUE=ovary;		
BCL2_RAT	RA	MEDLINE=95129487; PubMed=7828536;		
BCL2_RAT	RT	Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;		
BCL2_RAT	RT	"Expression of members of the bcl-2 gene family in the immature rat		
BCL2_RAT	RT	ovary: equine chorionic gonadotropin-mediated inhibition of granulosa		
BCL2_RAT	RT	cell apoptosis is associated with decreased bax and constitutive		
BCL2_RAT	RT	bcl-2 and bcl-xlmg messenger ribonucleic acid levels.";		
BCL2_RAT	RT	Endocrinology 136:232-241(1995).		
BCL2_RAT	RT	[3]		
BCL2_RAT	NP	SEQUENCE OF 19-172 FROM N.A.		
BCL2_RAT	RA	MEDLINE=95059917; PubMed=7969891;		
BCL2_RAT	RT	Castren E., Ohga Y., Bertzagli M.P., Tzimagiorgis G., Thoenen H.,		
BCL2_RAT	RT	Lindholm D.;		
BCL2_RAT	RT	"bcl-2 messenger RNA is localized in neurons of the developing and		
BCL2_RAT	RT	adult rat brain.";		
BCL2_RAT	RT	Neuroscience 61:165-177(1994).		
BCL2_RAT	RT	-1- FUNCTION: Suppresses apoptosis in a variety of cell systems		
BCL2_RAT	RT	including factor-dependent lymphohematopoietic and neural cells.		
BCL2_RAT	RT	Regulates cell death by controlling the mitochondrial membrane		
BCL2_RAT	RT	permeability. Appears to function in a feedback loop system with		
BCL2_RAT	RT	caspases. Inhibits caspase activity either by preventing the		
BCL2_RAT	RT	release of cytochrome c from the mitochondria and/or by binding to		
BCL2_RAT	RT	the apoptosis-activating factor (APAF-1).		
BCL2_RAT	RT	-1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and		
BCL2_RAT	RT	Bcl-xL). Heterodimerization with BAX requires intact BH1 and BH2		
BCL2_RAT	RT	domains, and is necessary for anti-apoptotic activity (By		
BCL2_RAT	RT	similarity). Also interacts with APAF-1 and RAIF-1 (By similarity).		
BCL2_RAT	RT	-1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular		
BCL2_RAT	RT	membrane of the nuclear envelope and the endoplasmic reticulum.		
BCL2_RAT	RT	-1- TISSUE SPECIFICITY: Expressed in a variety of tissues, with		
BCL2_RAT	RT	highest levels in reproductive tissues. In the adult brain,		
BCL2_RAT	RT	expression is localized in mitral cells of the olfactory bulb,		
BCL2_RAT	RT	granule and pyramidal neurons of hippocampus, pontine nuclei,		
BCL2_RAT	RT	cerebellar granule neurons, and in ependymal cells. In prenatal		

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CC brain, expression is higher and localized in the neuroepithelium
CC and in the cortical plate.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAF-1 (By similarity).
CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle. In the absence of
CC growth factors, ERKs and stress-activated kinases.
CC Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity (By similarity).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L14680; AAA53662.1; -
DR EMBL: U34964; AAA7687.1; -
DR EMBL: S74122; -; NOT_ANNOTATED_CDS.
DR HSSP: Q07817; IMAZ.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR003093; BCL2_BH4.
DR InterPro: IPR004725; BCL2_Reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfams: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS50063; BH4_2; 1.
KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
FT DOMAIN 10 30 BH4.
FT DOMAIN 90 104 BH3.
FT DOMAIN 133 152 BH1.
FT DOMAIN 184 199 BH2.
FT TRANSMEM 209 230 POTENTIAL.
FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY PKC) (BY SIMILARITY).
FT MOD_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
FT CONFLICT 42 42 A -> R (IN REF. 2).
FT CONFLICT 157 157 E -> G (IN REF. 1).
FT CONFLICT 164 164 S -> Y (IN REF. 2).
FT CONFLICT 212 212 L -> Q (IN REF. 2).
SQ SEQUENCE 236 AA; 26622 MW; E7688CB9071A872A CAC64;
Query Match 15.2%; Score 167.5; DB 1; Length 236;
Best Local Similarity 23.3%; Pred. No. 5.9e-08;
Matches 52; Conservative 36; Mismatches 78; Indels 57; Gaps 8;
QY 28 VAOKKAG-----REVYHARLRAGLSW-----SAPERASPARG----- 61
DB 1 MAQAGRGYDNRRELYMKIHKLSRGYEMTDGDSAPLRAAPPGLFSGPESNRTPA 60
QY 62 -----GRLAECVYLLRLGDELQIRPSYRNVAR-----OLHI-P 96
DB 61 VHRDTAATSPRLPLVANAAGPALSPVPVYHLTLRAGDDPSRRRYRDPFAEMSSQHLHP 120

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QY 97 I0SEPVYDAFLAVAGHIFSGITGWKVSIXSAAAGLAVDCVROAPAMHATVDCGE 156
DB 121 FLAR-----GRAFTVVEELFRQGVNMGRIYAFEPFGVNCVEVNMSPVDNIMKMT 176
QY 157 EVKRLATWLRRRGWTDLKCV-VSTRPGRSHWL-VATLCS 197
DB 177 YNRLHFWIIONGWDAFVELYGPSMRPLDFPWSLSIKTLIS 219
RESULT 2
BCL2_BOVIN STANDARD: PRT; 229 AA.
AC 002718;
DR 16-OCT-2001 (Rel. 40, Created)
DR 16-OCT-2001 (Rel. 40, Last sequence update)
DR 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Bos taurus (bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Holstein; TISSUE=Thymus;
RA Reyes R.A., Cockerell G.L.;
RT "Bovine leukemia virus associated-leukemogenesis is correlated
RT with suppression of programmed cell death and increased expression
RT of Bcl-2."
RL Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1) (By similarity).
CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity (By
CC similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum (By
CC similarity).
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAF-1 (By similarity).
CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle (By similarity). In
CC the absence of growth factors, Bcl2 appears to be phosphorylated
CC by other protein kinases such as ERKs and stress-activated
CC kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By
CC similarity).
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity (By similarity).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL: U92434; AAB53319.1; -
DR HSSP: 007817; 1MA2.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PR02180; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFS: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PS50063; BH4-2; 1.
DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
KW DOMAIN 10 30 BH4.
FT DOMAIN 64 68 POLY-PRO.
FT DOMAIN 69 72 POLY-ALA.
FT DOMAIN 83 97 BH3.
FT DOMAIN 126 145 BH1.
FT DOMAIN 177 192 BH2.
FT TRANSMEM 202 223 BH2.
FT SITE 34 35 CLEAVAGE (BY CASPASES).
FT MOD_RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ SEQUENCE 229 AA; 25099 MW; ADIDD0MF98FFI1D CRC64;

Query Match 15.0%; Score 164.5; DB 1; Length 229;
Best Local Similarity 23.1%; Pred. No. 1.1e-07;
Matches 49; Conservative 36; Mismatches 76; Indels 51; Gaps 7;

QY 37 EYHARILRLKGLSW-----SAPERASPARG-----GRAAE----- 66
DB 17 KYIHYKLSQNGYMGADAGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAP 76
QY 67 -----VCYVLRIGDELQIRPSYVYRNVAROLHI-PLQSEPVYTDALFVAGHIFGAGI 119
DB 77 SPPPPVYHLLTRQAGDDFSRRYRRDRFAEMSSQLHLTPFAR-----EFATVVEELFPDGV 132
QY 120 TWGKVVSLXSAAGLAVCYRQAPAVNALVDCLGFEFKRTLATWLRRGWTDVLKCV 179
DB 133 NMGRIVAFEEFGVCMCEVSNNREMSPLVDISALMPTFELNRHLHTWQDNGMDAFVELY 192
QY 180 -VSTKGFGRSHMLVATLCSGRFLKAAFFLL 210
DB 193 GFSMRPLDFFSWL-----SLKALLSLAL 215

RESULT 3
BCL2_CRIL0 STANDARD; PRT; 236 AA.
ID BCL2_CRIL0
AC Q9JVB8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OC NCBI_TaxID=10030;
RN NCBI_TaxID=10030;
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=20431763; PubMed=10973819;
RA Tomicic M.T., Kaina B.;
RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2
RT protein.";
RL Biochem. Biophys. Res. Commun. 275:899-903(2000).

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RN [2]
RP SEQUENCE FROM N.A. AND CLEAVAGE BY CASPASES.
RX MEDLINE=21092839; PubMed=11181062;
RA Tomicic M.T., Kaina B.;
RT "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9
RT and caspase-3.";
RL Biochem. Biophys. Res. Commun. 281:404-408(2001).
CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1) (By similarity).
CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity (By
CC similarity). Also interacts with APAF-1 and RA-1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RA-1 (By similarity).
CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle (By similarity). In
CC the absence of growth factors, Bcl2 appears to be phosphorylated
CC by other protein kinases such as ERKs and stress-activated kinases
CC (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A)
CC (By similarity).
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC
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CC or send an email to license@sdb.ch).
CC -----
DR EMBL: AJ271720; CAB92245.1; -
DR HSSP: 007817; 1MA2.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFS: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PS50063; BH4-2; 1.
DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
KW DOMAIN 10 30 BH4.
FT DOMAIN 64 68 BH3.
FT DOMAIN 69 72 BH1.
FT DOMAIN 133 152 BH1.
FT DOMAIN 184 199 BH2.
FT TRANSMEM 209 230 BH2.
FT SITE 64 65 POTENTIAL.
FT MOD_RES 70 70 CLEAVAGE (BY CASPASE-3 AND CASPASE-9).
FT PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

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SQ SEQUENCE 236 AA; 26491 MW; BECADPTEF337228 CRC64;  
 Query Match 14.5%; Score 159.5; DB 1; Length 236;  
 Best Local Similarity 22.4%; Pred. No. 3e-07;  
 Matches 50; Conservative 37; Mismatches 79; Indels 57; Gaps 8;

QY 28 VQAKRLG-----KEYHARLRLRGLSW-----SAPERASPAG----- 61  
 DB 1 MAQAGTGDNRREIYMKYHYKISQGYEMDVGDDAALGAPRGIFSFQESNPTRA 60  
 QY 62 -----GRLAEVCTVLRIGDELEQIRPSVYRNVAR-----QLHI-P 96  
 DB 61 VHRDMAFRSPLRPVATGPTLSPVPVYHLTLRRAGDQFSRRYRDRFAEMSSQHLTP 120  
 QY 97 LOSEPVTDAFLAVAGHITSAGITGKVVSLYSAAGLAVDCVROAPMVAHALDCLGE 156  
 DB 121 FTAR-----GRFAVVELELFRDGMGRIVAFEFEGVCMCEVSNNRMSPLVDNALMTE 176  
 QY 157 FVRKTLATWLRRRGCGWTDVLCV-VSTRKGFRRSHL-VATLCS 197  
 DB 177 YLNRHLHTWIQDNGMDAFVELYGPVRPLDFRSWLSTLTL 219

RESULT 4  
 BCL2\_MOUSE STANDARD; PRT; 236 AA.  
 AC P10417; P10418;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2 OR BCL-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RC STRAIN=BAIB/C; TISSUE=Liver;  
 RX Neglin M., Sillini E., Kozak C., Tsujimoto Y., Croce C.M.;  
 RT "Molecular analysis of bcl-2: structure and expression of the murine  
 RT gene homologous to the human gene involved in follicular lymphoma.",  
 RL Cell 49:455-463(1987).  
 RN [2]  
 RP REVISIONS TO 221-222.  
 RX MEDLINE=92375724; PubMed=1508712;  
 RA Eguchi Y., Ewert D.L., Tsujimoto Y.;  
 RT "Isolation and characterization of the chicken bcl-2 gene: expression  
 RT in a variety of tissues including lymphoid and neuronal organs in  
 RT adult and embryo.";  
 RL Nucleic Acids Res. 20:4187-4192(1992).  
 RN [3]  
 RP PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.  
 RX MEDLINE=97277291; PubMed=9115213;  
 RA "Ito T., Deng X., Carr B., May W.S. Jr.;  
 RT "Bcl-2 phosphorylation required for anti-apoptosis function.";  
 RL J. Biol. Chem. 272:11671-11673(1997).  
 RN [4]  
 RP DEPHOSPHORYLATION BY PP2A.  
 RX MEDLINE=99069407; PubMed=9852076;  
 RA Deng X., Ito T., Carr B., Mumbly M., May W.S. Jr.;  
 RT "Reversible phosphorylation of Bcl2 following Interleukin 3 or  
 RT bryostatins 1 is mediated by direct interaction with protein  
 RT phosphatase 2A\*";  
 RL J. Biol. Chem. 273:34157-34163(1998).  
 CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (APAF-1).

CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
 CC domains, and is necessary for anti-apoptotic activity (by  
 CC domain). Also interacts with APAF-1 and RAIF-1.  
 CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;  
 CC are produced by alternative splicing.  
 CC -!- TISSUE SPECIFICITY: Expressed in a variety of tissues.  
 CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 CC for interaction with RAIF-1.  
 CC -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle. In the absence of  
 CC growth factors, Bcl2 appears to be phosphorylated by other protein  
 CC kinases such as ERKs and stress-activated kinases.  
 CC -!- Dephosphorylated by protein phosphatase 2A (PP2A).  
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity.  
 CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----

DR EMBL: L31532; AAA37282.1; -;  
 DR EMBL: M16506; AAA37282.1; JOINED.  
 DR EMBL: M16506; AAA37281.1; -;  
 DR PIR: A25960; TVMSA1.  
 DR PIR: B25960; TVMSA1.  
 DR PIR: E37332; E37332.  
 DR HSSP: 007817; 1MA2.  
 DR MGD: MGI:88138; Bcl2.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR007112; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH4.  
 DR InterPro: IPR004725; BCL2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 DR Apoptosis; Alternative splicing; Transmembrane; Mitochondrion;  
 KW Phosphorylation.  
 FT DOMAIN 10 30 BH4.  
 FT DOMAIN 90 104 BH3.  
 FT DOMAIN 133 152 BH1.  
 FT DOMAIN 184 199 BH2.  
 FT TRANSMEM 209 230 POTENTIAL.  
 FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
 FT MOD.RES 70 70 PHOSPHORYLATION (BY PKC).  
 FT VARSPPLIC 193 236 DAFVELGSPRPLDFESWLSTLALVACITLGAYL  
 FT GHK -> VGACILE (IN ISOFORM BETA).  
 SQ SEQUENCE 236 AA; 26425 MW; AA85FE6B0766BEDA CRC64;  
 Query Match 14.3%; Score 157.5; DB 1; Length 236;

Best Local Similarity 22.4%; Pred. No. 4.6e-07;  
Matches 50; Conservative 37; Mismatches 79; Indels 57; Gaps 8;

OY 28 VQAQAKLG-----REYVAKRLRAGLSW-----SAPRRASAPG-----61  
Db 1 MAQAGRGYDNRREIVMKYIHYKLSORGEWDADADADAAPGAAPGICFSGFQESNMPA 60  
OY 62 -----GRLAEVCTVLLRLDELEQIRPSYRVNAR-----QLHI-P 96  
Db 61 VHEEMAKRISPLRLPVATAGPALSPPVPCVHLTLRRAGDPSRRYRRDFAMSSQLHLTP 120  
OY 97 LQSEPVYTDALFVAGHIFSGITWGRKVSLSYSAAGLAVDCYRQAPAMVHALVDCLGE 156  
Db 121 FTAR-----GREATVEELFRDGVNMGRIVAFEEFGVGVCESVNREKSPLYNDIALMTE 176  
OY 157 FVKRTLATWLRRGGRWTLKCV-VSTKPGFRSHML-VAILCS 197  
Db 177 YLNRHLHTWIDNGMDAFVELYGPMSRPLDFESWLSKTLIS 219

## RESULT 5

ARL\_XENLA  
ID ARL\_XENLA STANDARD; PRT; 228 AA.  
AC 091827;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptosis regulator R1 (XRL) (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
OC Xenopodinae; Xenopus.  
NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Head;  
RX MEDLINE=95331613; PubMed=7607538;  
RA Cruz-Reyes J., Tata J.R.;  
RT "Cloning, characterization and expression of two Xenopus bcl-2-like  
RT cell-survival genes".  
RT Gene 158:171-179(1995).  
RL  
CC -1- FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W.  
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).  
CC -1- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE  
CC BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND  
CC ADULTS. WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC -----  
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CC -----  
DR EMBL: X82462; CA57845.1; -  
DR HSSP: Q07817; 1MAZ.  
DR InterPro: IPR002475; BCL2\_family.  
DR InterPro: IPR000712; Bcl2\_BH.  
DR InterPro: IPR003093; Bcl2\_BH4.  
DR Pfam: PF00452; Bcl-2; 1.  
DR Pfam: PF02180; BH4; 1.  
DR SMART: SM00337; BCL; 1.  
DR SMART: SM00265; BH4; 1.  
DR PROSITE: PS01080; BH1; 1.  
DR PROSITE: PS01258; BH2; 1.  
DR PROSITE: PS00062; BCL2\_FAMILY; 1.  
KM Apoptosis; Transmembrane.  
FT NON\_TER 1  
FT DOMAIN 120 139 BH1.

FT DOMAIN 171 186 BH2.  
FT TRANSMEM 207 227 POTENTIAL.  
SQ SEQUENCE 228 AA; 25068 MM; C499DD449A585F8A9 CRC64;  
Matches 39; Conservative 35; Mismatches 71; Indels 20; Gaps 5;

Query Match 14.1%; Score 155; DB 1; Length 228;  
Best Local Similarity 23.6%; Pred. No. 7.4e-07;

OY 19 DRMPDKELVAAQ-----AKALGREYVAKRLRAGLSWAPRRASAPGRLAEVC---TVL 71  
Db 32 DKYTEEGMMAQSDLGSRALVEDLVRYKLCORSL-----VPEPSG--AASCAHSAM 81  
OY 72 LRLGDELEQIRPSYRVNARQLHPILOSEPVYTDALFVAGHIFSGITWGRKVSLSAA 131  
Db 82 RAODEFEERFRQAFSISQIHV---TPGTAAARFAEVAGSLFQGVNMGRIVAFRVFG 138  
OY 132 AGLAVDCYRQAPAMVHALVDCIEFVYKRTLATWLRRGGRWTL 176  
Db 139 AALCAESVNKEMSPLLPRIDMMVTVLETNLRDVIQNGMGNGPL 183

## RESULT 6

BCL2\_CHICK  
ID BCL2\_CHICK STANDARD; PRT; 233 AA.  
AC 000709;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DE 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptosis regulator Bcl-2.  
GN BCL2 OR BCL-2.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92375724; PubMed=1508712;  
RA Cazals-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;  
RT "Molecular cloning and DNA sequence analysis of cDNA encoding chicken  
RT homologue of the Bcl-2 oncoprotein".  
RT Biochim. Biophys. Acta 1132:109-113(1992).  
RL  
CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
CC including factor-dependent lymphohematopoietic and neural cells.  
CC Regulates cell death by controlling the mitochondrial membrane  
CC permeability. Appears to function in a feedback loop system with  
CC caspases. Inhibits caspase activity either by preventing the  
CC release of cytochrome c from the mitochondria and/or by binding to  
CC the apoptosis-activating factor (Apaf-1).  
CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
CC domains, and is necessary for anti-apoptotic activity (By  
CC similarity). Also interacts with Apaf-1 and Raf-1 (By similarity).  
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
CC membrane of the nuclear envelope and the endoplasmic reticulum.  
CC -1- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen,  
CC kidney, heart, ovary and brain, with the highest levels in the  
CC thymus. In the embryo, highly levels expressed in all tissues with  
CC high levels in the bursa of Fabricius.  
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
CC for interaction with Raf-1 (By similarity).  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.

```

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL: D11382; BAA01978.1;
DR EMBL: D11381; BAA01978.1; JOINED.
DR EMBL: Z11961; CA78018.1;
DR PIR: A37332; A37332.
DR PIR: S24390; S24390.
DR HSP: 007817; 1MA2.
DR InterPro: IPR002475; BCL2 family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH4.
DR InterPro: IPR004725; Bcl2_Reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfam: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PS50063; BH4_2; 1.
KW Apoptosis; Transmembrane; Mitochondrion.
FT DOMAIN 10 30 BH4.
FT DOMAIN 87 101 BH3.
FT DOMAIN 130 149 BH1.
FT DOMAIN 181 196 BH2.
FT TRANSMEM 208 228 POTENTIAL.
FT CONFLICT 64 64 E -> S (IN REF. 2).
FT CONFLICT 67 82 GSAASEVPPAEGLRP -> ARLLVRCPRRLGCA
      (IN REF. 2).
FT CONFLICT 121 121 H -> T (IN REF. 2).
FT CONFLICT 139 139 G -> V (IN REF. 2).
SQ SEQUENCE 233 AA; 25687 MW; 5252555ACB6EC3D CRC64;

Query Match 14.1%; Score 155; DB 1; Length 233;
Best Local Similarity 20.6%; Pred. No. 7.6e-07;
Matches 45; Conservative 36; Mismatches 81; Indels 56; Gaps 6;

OY 37 EYVHARLLRAGSWSA-----PERASPAAGRGRLAEVCT----- 69
DB 17 KTIHKLRSQGYDMAGDEPRPPAPAPAAVAAGAASSHHRPEPPGSAASEVPP 76
OY 70 -----VLRLEDELEQIRPSYRVNARQLH-PLQSEFVYDAFLAVAGHIF 115
DB 77 AEGLRPAPGVALRQAGDEFSRRYQRFQAGMSGLHPTFAH-----GRVAVAEELF 132
OY 116 SAGITWGKVVSLYSAAAGIADVCVQAOAPAMVHALVDCIEGVVKKTLATWLRRCGWDIV 175
DB 133 RDGVWNGRIVAFFEEGVCVSVNREMSPLVDNIATWTECINRHLNMIODNGMDAF 192
OY 176 LKCV-VSTRKPGFRSHW-----LVATLCSFGREL 202
DB 193 VELYGNMRLPFDPSMISLKTLLSLVLGACITLGAIVL 230

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DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI-TaxID-9606;
RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RX MEDLINE=86259760; PubMed=3523487;
RA Tsujimoto Y., Croce C.M.;
RT "Analysis of the structure, transcripts, and protein products of
RT bcl-2, the gene involved in human follicular lymphoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
RN [2]
RP REVISIONS TO 96; 110 AND 237.
RX MEDLINE=92375724; PubMed=1508712;
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression
RT in a variety of tissues including lymphoid and neuronal organs in
RT adult and embryo.";
RL Nucleic Acids Res. 20:4187-4192(1992).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=87002488; PubMed=2875799;
RA Cleary M.L., Smith S.D., Sklar J.;
RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-
RT 2/immunoglobulin transcript resulting from the t(14;18)
RT translocation.";
RL Cell 47:19-28(1986).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=88196071; PubMed=2834197;
RA Seto M., Jaeger U., Hockelt R.D., Granger W., Bennett S.,
RA Goldman P., Korsmeyer S.J.;
RT "Alternative promoters and exons, somatic mutation and deregulation
RT of the Bcl-2-Ig fusion gene in lymphoma.";
RL EMBO J. 7:123-131(1988).
RN [5]
RP SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS NHL.
RX MEDLINE=92096610; PubMed=1339299;
RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.;
RT "Frequent incidence of somatic mutations in translocated BCL2
RT oncogenes of non-Hodgkin's lymphomas.";
RL Blood 79:229-237(1992).
RN [6]
RP SUBCELLULAR LOCATION.
RX MEDLINE=91066924; PubMed=2250705;
RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.;
RT "Bcl-2 is an inner mitochondrial membrane protein that blocks
RT programmed cell death.";
RL Nature 348:334-336(1990).
RN [7]
RP MUTAGENESIS.
RX MEDLINE=94239528; PubMed=8183370;
RA Yin X.-M., Oltvai Z.N., Korsmeyer S.J.;
RT "BH1 and BH2 domains of Bcl-2 are required for inhibition of
RT apoptosis and heterodimerization with Bax.";
RL Nature 369:321-323(1994).
RN [8]
RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.
RX MEDLINE=98057466; PubMed=9395403;
RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,
RA Ueno K., Hardick J.M.;
RT "Conversion of Bcl-2 to a Bax-like death effector by caspases.";
RL Science 278:1966-1988(1997).
RN [9]
RP REVIEW ON PHOSPHORYLATION.
RX MEDLINE=21260650; PubMed=11368354;
RA Ruvoilo P.P., Deng X., May W.S.;
RT "Phosphorylation of Bcl2 and regulation of apoptosis.";
RL Leukemia 15:515-522(2001).
RN [10]
RP PHOSPHORYLATION BY ASK1/JNK1.

```







AC P53563; 062678; P70614; P70613; 062836; 064087; 064128;  
AD 01-OCT-1996 (Rel. 34, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptosis regulator Bcl-x.  
GN BCL2L1 OR BCL2L OR BCLX.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sclurognathii; Muridae; Murinae; Rattus  
OX NCBI\_TaxID-10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).  
RC TISSUE=Brain;  
RA Michaelidis T.M.;  
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Messelings S.L., David G.L., Choi S., Veliuona M., Hardwick J.M.;  
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).  
RC TISSUE=Thymus;  
RA [3]  
RL [3]  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).  
RC STRAIN=Sprague-Dawley; TISSUE=OVARY;  
RX MEDLINE-95129487; PubMed-7828536;  
RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;  
RT "An additional form of rat Bcl-x, Bcl-x(beta), generated by an  
RT unspliced RNA, promotes apoptosis in promyeloid cells.";  
RL J. Biol. Chem. 271:13258-13265(1996).  
RL [4]  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).  
RC STRAIN=Sprague-Dawley; TISSUE=OVARY;  
RX MEDLINE-95129487; PubMed-7828536;  
RA Atiomi M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,  
RA Morikawa K.;  
RT "Crystal structure of rat Bcl-xL. Implications for the function of  
RT the Bcl-2 protein family.";  
RL J. Biol. Chem. 272:27886-27892(1997).  
CC -1 FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
CC caspases (By similarity). Appears to regulate cell death by  
CC blocking the voltage-dependent anion channel (VDAC) by binding  
CC to it and preventing the release of the caspase activator.  
CC cytochrome c, from the mitochondrial membrane. The Bcl-x(s) and  
CC Bcl-x(beta) isoforms promote apoptosis.  
CC -1 SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By  
CC similarity). Heterodimerization with BAX does not seem to be  
CC required for anti-apoptotic activity (By similarity).  
CC -1 SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
CC ENVELOPE (By similarity).  
CC -1 ALTERNATIVE PRODUCTS: 3 ISOFORMS: BCL-X(L) (SHOWN HERE), BCL-X(S)  
CC AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1 TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS  
CC SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE  
CC OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT  
CC DETECTABLE LEVEL OF BCL-X(S).  
CC -1 DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
CC The BH1 and BH2 domains are required for both heterodimerization  
CC with other Bcl2 family members and for repression of cell death.  
CC -1 PTM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleaved proteolite, lacking the BH4 domain, has pro-apoptotic  
CC activity (By similarity).  
CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.

```

CC -I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X82537; CAAS7886.1; -
DR EMBL: X82537; CAAS7887.1; -
DR EMBL: U10579; AAA19257.1; -
DR EMBL: U72349; AAB17353.1; -
DR EMBL: U72349; AAB17352.1; -
DR EMBL: U34963; AAA77686.1; -
DR EMBL: S76513; AAC60701.1; ALT_INIT.
DR EMBL: S78284; AAC60702.1; -
DR PDB: 1AF3; 07-JUL-97.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR003093; BCL2_BH4.
DR InterPro: IPR004725; BCL2_Reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfams: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS50063; BH4_2; 1.
KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
KW 3D-structure.
FT DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.
FT DOMAIN 180 195 BH2.
FT TRANSMEM 210 226 POTENTIAL.
FT TRANSMEM 126 188 MISSING (IN ISOFORM BCL-X(S)).
FT VASAPLIC 189 233 DTPVDLGNNAASERKQEPNRFELTGMVYAGVILGSL
FT VASAPLIC 189 233 FSRK -> VRTPLVCPPLVCLSSVEIPNCPMSGVAVED
FT FT IDYSGDIPGLL (IN ISOFORM BCL-X(BETA)).
FT FT R -> Q (IN REF. 1).
FT FT F -> S (IN REF. 2).
FT FT A -> E (IN REF. 2).
FT FT I -> L (IN REF. 4).
FT FT A -> V (IN REF. 4).
FT FT FF -> SS (IN REF. 4).
FT FT A -> T (IN REF. 4).
FT FT A -> P (IN REF. 4).
SQ SEQUENCE 233 AA; 26158 MW; 2B62B6C3864BCBF CRC64;

Query Match 13.7%; Score 150.5; DB 1; Length 233;
Best Local Similarity 22.1%; Pred. No. 1.9e-06;
Matches 43; Conservative 29; Mismatches 66; Indels 55; Gaps 5.

23 TDKEIVAAQAKLGREYVARLLRAGLSWS-----APERA----- 56
Db 4 SNRELIVY-----DFLSYKLSQKQYSMSQSFDEVENTEADEETPERETPSALINGNS 56

57 -----SPAPGR-----LAECTVLLRLGDELQIRPSYRYNVAROLHPL 97
Db 57 WHLSDPVCNATGSHSSLDAREVIPMAVQAOLREADDEFLRYRAFSDLTSLHI-- 114

98 OSEPVNTAPFLAVAGHIFPSAGITGWKVVSLVSAAGLAVDCVROQAPAWVHALVCLGEF 157
Db 115 -TPGAIVSDFQVYNVELPRDGVNMGRIVAFPSFGALCVESYDKEMQVLVSKIASMATY 173

158 VRKTLATWLRRRGW 172

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Db 174 LNDHLEPMIOENGM 188

RESULT 10

ID	BAXB_HUMAN	STANDARD	PRT	218 AA
AC	007814			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Apoptosis regulator BAX, cytoplasmic isoform beta.			
GN	BAX.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=B-cell;			
RX	MEDLINE=93364978; PubMed=8358790;			
RA	Olival Z.N., Millman C.L., Korsmeyer S.J.;			
RT	"Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates programmed cell death.";			
RL	Cell 74:609-619(1993).			
CC	-1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADONOVIRUS HOMOLOG E1B 19K PROTEIN.			
CC	-1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.			
CC	-1- E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.			
CC	-1- DOMAIN: INTERACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.			
CC	CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.			
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.			
CC	-----			
CC	CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; L22474; AAA03620.1; -			
DR	PIR; B47538; B47538.			
DR	HSSP; 007817; IMAZ.			
DR	GENEW; HGNC:959; BAX.			
DR	MTM; 600040.			
DR	InterPro; IPR002475; BCL2_family.			
DR	InterPro; IPR000712; BCL2_BH.			
DR	Pfam; PF00452; Bcl-2; 1.			
DR	SMART; SM00337; BCL; 1.			
DR	PROSITE; PS01080; BH1; 1.			
DR	PROSITE; PS01258; BH2; 1.			
DR	PROSITE; PS01259; BH3; 1.			
DR	PROSITE; PSS0062; BCL2_FAMILY; 1.			
DR	APOLIS; Alternative splicing.			
FT	DOMAIN 59 73 BH3.			
FT	DOMAIN 98 118 BH1.			
FT	DOMAIN 150 165 BH2.			
SO	SEQUENCE 218 AA; 24220 MW; F69DCD70F960192F CRC64;			

Query Match 13.5%; Score 148.5; DB 1; Length 218;  
 Best Local Similarity 28.8%; Pred. No. 2,7e-06;  
 Matches 46; Conservative 72; Indels 13; Gaps 6;

Db 174 LNDHLEPMIOENGM 188

RESULT 11

ID	BCLX_HUMAN	STANDARD	PRT	233 AA
AC	007817			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Apoptosis regulator Bcl-x.			
GN	BCL2L1 OR BCL2L OR BCLX.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).			
RX	MEDLINE=93364977; PubMed=8358789;			
RA	Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,			
RT	Turka L.A., Mao X., Nunez G., Thompson C.B.;			
RT	"bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic cell death.";			
RL	Cell 74:597-608(1993).			
CC	[2]			
CC	CC SEQUENCE FROM N.A. (ISOFORM BETA).			
CC	CC Inohara N., Ohta S.;			
CC	CC Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.			
CC	[3]			
CC	CC MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.			
CC	RX MEDLINE=95372373; PubMed=7644501;			
CC	CC Sedlak T.W., Olival Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,			
CC	CC Korsmeyer S.J.;			
CC	CC "Multiple Bcl-2 family members demonstrate selective dimerizations with Bax.";			
CC	CC Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).			
CC	[4]			
CC	CC MUTAGENESIS OF BH1 AND BH2 DOMAINS.			
CC	RX MEDLINE=96170038; PubMed=859636;			
CC	CC Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,			
CC	CC Korsmeyer S.J.;			
CC	CC "Bax-independent inhibition of apoptosis by Bcl-XL.";			
CC	CC Nature 379:554-556(1996).			
CC	[5]			
CC	CC STRUCTURE BY NMR OF 1-209.			
CC	RX MEDLINE=97117562; PubMed=9020082;			
CC	CC Sattler M., Liang H., Nettlesheim D., Meadows R.P., Harlan J.E.,			
CC	CC Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,			
CC	CC Thompson C.B., Fesik S.W.;			
CC	CC "Structure of Bcl-XL-Bax peptide complex: recognition between regulators of apoptosis.";			
CC	CC Science 275:983-986(1997).			
CC	[6]			
CC	CC X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.			
CC	RX MEDLINE=9625675; PubMed=8692274;			
CC	CC Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,			
CC	CC Yoon H.S., Nettlesheim D., Chang B.S., Thompson C.B., Wong S.L.,			
CC	CC Ng S.L., Fesik S.W.;			
CC	CC "X-ray and NMR structure of human Bcl-XL, an inhibitor of programmed cell death.";			
CC	CC Nature 381:335-341(1996).			
CC	[7]			

RP CLEAVAGE BY CASPASES, AND MUTAGENESIS OF ASP-61.  
 RX MEDLINE-98118550; PubMed-9435230;  
 RA Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.,  
 RA Takahashi A., Kasan M.B., Griffin D.E., Earshaw W.C., Veluona M.A.,  
 RA Hardwick J.M.,  
 RT "Modulation of cell death by Bcl-XL through caspase interaction."  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).  
 CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (by similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane. The Bcl-X(S)  
 CC isoform promotes apoptosis.  
 CC -1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2.  
 CC Heterodimerization with BAX does not seem to be required for anti-  
 CC apoptotic activity.  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
 CC ENVELOPE (BY SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S)  
 CC AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS  
 CC THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING  
 CC LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING  
 CC LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.  
 CC -1- DOMAIN: The B44 domain is required for anti-apoptotic activity.  
 CC The B41 and B42 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the B44 domain, has pro-apoptotic  
 CC activity.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (B41) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (B42) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (B43) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (B44) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: 223116; CA80662.1; -  
 DR EMBL: 223115; CA80661.1; -  
 DR EMBL: U72398; AAB17354.1; -  
 DR PDB: 1BXL; 29-OCT-97.  
 DR PDB: 1LXL; 21-APR-97.  
 DR PDB: 1MAZ; 21-APR-97.  
 DR Genew: HGNC:992; BCL2L1.  
 DR MIM: 600039; -  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; B44; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRfam: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1.  
 DR PROSITE: PS00563; BH4\_2; 1.  
 KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;  
 KW 3D-structure.  
 FT DOMAIN 4 24 BH4.  
 FT DOMAIN 86 100 BH1.  
 FT DOMAIN 129 148 BH1.  
 FT DOMAIN 180 195 BH2.

FT TRANSMEM 210 226 POTENTIAL.  
 FT SITE 61 61 CLEAVAGE BY CASPASE-1.  
 FT VARSPIC 126 188 MISSING (IN ISOFORM BCL-X(S)).  
 FT VARSPIC 189 233 DTFVELGNNAAESRRGQENRNEFLGTGAVGVLGSL  
 FT ESKR -> VTRKPLVCPFLASGSRFTALLVFLCWVI  
 FT VGDVDS (IN ISOFORM BCL-X(BETA)).  
 FT D->A: NO CLEAVAGE BY CASPASE-1 NOR BY  
 FT CASPASE-3.  
 FT FRD->A: NO HETERO-DIMERIZATION WITH BAX.  
 FT VMN->A: LOSS OF ANTI-APOPTOTIC  
 FT ACTIVITY.  
 FT GRI->ELN: LOSS OF ANTI-APOPTOTIC  
 FT ACTIVITY.  
 FT G->A: NO HETERO-DIMERIZATION WITH BAX.  
 FT G->E: NO HETERO-DIMERIZATION WITH BAX.  
 FT D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY  
 FT BY ABOUT HALF.  
 FT D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT G->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT FT CONFLICT 70 70  
 SO SEQUENCE 233 AA; 26049 MM; E09D3CDD851AE9BE CRC64;  
 Query Match 13.3%; Score 146.5; DB 1; Length 233;  
 Best Local Similarity 22.1%; Pred. No. 4.3e-06;  
 Matches 43; Conservative 29; Mismatches 68; Indels 55; Gaps 5;  
 QY 23 TDKEIVAAQALRGREYVHAHLRAGLSMS-----APEAA----- 56  
 DB 4 SNRELVA-----DELSTKLSQSGVMSQPSDVENRENTAPEETSEMETPSAINCPNS 56  
 QY 57 -----SPAPGGR-----LAECVTLLRLGDELEDIRSVYNNVAROLHPL 97  
 DB 57 WHLADSPAVNGAGHGSSLDAREVYPAAYKQALRENGDEFELRYRAFFDLTSQLHI-- 114  
 QY 98 QSEPVYTDFAFLAVAGHIFSGITGKGVSLYSAAGLAIVDCVROQAPAMVHALVDCGEF 157  
 DB 115 -TGTAYOSFEQVYNELFRDGVNMGRIYAFPSGALCVESYDKEMQVLSRIAMATY 173  
 QY 158 VRKLTATWLRRGGM 172  
 DB 174 LNDHLEPWIQENGGM 188  
 RESULT 12  
 BCLX\_PIG STANDARD; PRT; 233 AA.  
 AC 07737;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-x.  
 GN BCL2L1 OR BCL2L OR BCLX.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99171363; PubMed-10072723;  
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Diermer D.;  
 RT "Quantification of cardioprotective gene expression in porcine  
 RT short-term hibernating myocardium."  
 RL J. Mol. Cell. Cardiol. 31:147-158(1999).  
 CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (by similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane.  
 CC -1- SUBUNIT: Bcl-X(L) forms heterodimers with BAX, BAK and Bcl-2 (By  
 CC similarity). Heterodimerization with BAX does not seem to be  
 CC required for anti-apoptotic activity (by similarity).  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR

CC ENVELOPE (BY SIMILARITY).  
 CC -I- DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
 CC The BH1 and BH2 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -I- PPM: Prototypically cleaved by caspases during apoptosis (by  
 CC similarity). The cleaved protein, lacking the BH4 domain, has pro-  
 CC apoptotic activity (by similarity).  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AJ001203; CAA04597.1; -  
 CC HSSP: Q07817; 1MA2.  
 DR InterPro: IPR002475; BCL2 family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRfam: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS00062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS00063; BH4\_2; 1.  
 DR Apoptosis; Mitochondrion; Transmembrane.  
 KM DOMAIN 4 24 BH4.  
 FT DOMAIN 86 100 BH3.  
 FT DOMAIN 129 148 BH1.  
 FT DOMAIN 180 195 BH2.  
 FT TRANSMEM 210 226 POTENTIAL.  
 SQ SEQUENCE 233 AA: 26061 MW: 18566 RA0441912B2 CRC64;  
 Query Match 13.3%; Score 146.5; DB 1; Length 233;  
 Best Local Similarity 22.1%; Pred. No. 4.3e-06;  
 Matches 43; Conservative 29; Mismatches 68; Indels 55; Gaps 5;  
 QY 23 TRKELVAKKALGREYVHARLRAGISMS-----ADPERA----- 56  
 DB 4 SNRELTV-----DFLSYKLSQKGSWSQFTDVEENRTAEDEGESEAEFSAINGNS 56  
 QY 57 -----SPARGR-----LAECVTLRLGDELDIRSVRYNAROLHPL 97  
 DB 57 WILADSPAYNGATGSSSDAREVPMAYVKQALRPADEFEELRRRAISDLISQHLT-- 114  
 QY 98 QSEPVVTDALVAGHIFSGITGKRVSLYSAAGLAVDCVROAPAVVHNLVDCIGEF 157  
 DB 115 -TPGTAVGSEFQVNLNLFEDGVNMGRIYVAFSEGCALCVESDKENQVLSIATIMATY 173  
 QY 158 VKTTLATWLRRCGW 172  
 DB 174 LNDHLEPWIOENGW 188  
 RESULT 13  
 BAXA\_HUMAN  
 ID BAXA\_HUMAN STANDARD: PRT; 192 AA.  
 AC Q07812;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator BAX, membrane isoform alpha.  
 GN BAX.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 ON NCBI\_TaxID=9606;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-B-cell;  
 RX MEDLINE=93364978; PubMed=8358790;  
 RA Olvay Z.N., Millman C.L., Korsmeyer S.J.;  
 RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that  
 RT accelerates programmed cell death.";  
 RL Cell 74:609-619(1993).  
 RN [2]  
 RP MUTAGENESIS. AND FUNCTION OF BH3 DOMAIN.  
 RX MEDLINE=96091131; PubMed=8521816;  
 RA Childenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,  
 RA Elangovan B., Chinnadurai G., Lutz R.J.;  
 RT "A conserved domain in Bax, distinct from BH1 and BH2, mediates cell  
 RT death and protein binding functions.";  
 RL EMBO J. 14:5589-5596(1995).  
 RN [3]  
 RP VARIANT PLASMACYTOMA GLU-11, VARIANT T-CELL ACUTE LYMPHOBLASTIC  
 RP LEUKEMIA ARG-67, AND VARIANT BURKITT LYMPHOMA VAL-108.  
 RX MEDLINE=98200607; PubMed=9531611;  
 RA Meijerink J.P.P., Mensink E.J.B.M., Wang K., Sedlak T.W.,  
 RA Sloetjes A.W., de Witte T., Waksman G., Korsmeyer S.J.;  
 RT "Hematopoietic malignancies demonstrate loss-of-function mutations of  
 RT BAX.";  
 RL Blood 91:2991-2997(1998).  
 CC -I- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND  
 CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS  
 CC HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,  
 CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.  
 CC -I- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,  
 CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.  
 CC -I- SUBCELLULAR LOCATION: Membrane-bound.  
 CC -I- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE  
 CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY  
 CC ALTERNATIVE SPLICING.  
 CC -I- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  
 CC -I- DOMAIN: INTRACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND  
 CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION  
 CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.  
 CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.  
 CC -I- DISEASE: Defects in BAX are found in some cell lines from  
 CC hematopoietic malignancies as T-cell acute lymphoblastic leukemia,  
 CC Burkitt lymphoma, and plasmacytoma.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: L22473; AAA03619.1; -  
 DR PIR: A47538; A47538.  
 DR HSSP: Q07817; 1MA2.  
 DR Genew: HGNC:959; BAX.  
 DR MIM: 600040;  
 DR InterPro: IPR002475; BCL2 family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS00062; BCL2\_FAMILY; 1.

CC	DR	PROSITE; PS01080; BH1; 1.
CC	DR	PROSITE; PS01258; BH2; 1.
CC	DR	PROSITE; PS01259; BH3; 1.
CC	KW	Apoptosis; Anti-oncogene; Transmembrane; Alternative splicing;
CC	KW	Disease mutation.
CC	FT	DOMAIN 59 73 BH3.
CC	FT	DOMAIN 98 118 BH1.
CC	FT	DOMAIN 150 165 BH2.
CC	FT	TRANSMEM 172 192 POTENTIAL.
CC	FT	VARIANT 11 11 G->E (IN PLASMACYTOMA).
CC	FT	/FTID=VAR_013575.
CC	FT	G->R (IN T-CELL ACUTE LYMPHOBLASTIC
CC	FT	LEUKEMIA; LOSS OF HETERODIMERIZATION WITH
CC	FT	BCL-2 OR BCL-X(L)).
CC	FT	/FTID=VAR_007809.
CC	FT	G->V (IN BURKITT LYMPHOMA; LOSS OF
CC	FT	HOMODIMERIZATION).
CC	FT	/FTID=VAR_013576.
CC	SO	SEQUENCE 192 AA; 21184 MW; 6C0CB0A7DEFA4994 CRC64;
CC	QY	Query Match 13.0%; Score 143.5; DB 1; Length 192;
CC	Db	Best Local Similarity 28.3%; Pred. No. 6.4e-06;
CC	Matches	45; Conservative % 29; Mismatches 72; Indels 13; Gaps 6;
CC	QY	22 PTDDELVAQAALGRE-VYHARLLRAGLSMSAPERA-SFAP-GGRLAECYVLNLGDEL 78
CC	Db	13 PTSSQIKTKTGAALLQGFIIDPRAGRMG--GEAPELADPPVPDASTKRKLSCEIKRIGDEL 70
CC	QY	79 EQIRPSRYRNARQLHIPOSEPVYTDAPFLAVAGHIFSG-IITGWKVSLYSAAGLAVD 137
CC	Db	71 DS-----NMELQRMIATVDTPDSREFFFRVAAMAFEDSGNFNMGRRVALPFPASKLYLK 123
CC	QY	138 CVROAQPMVAHVADVLCGEFYVKTLTAWLRRRGWTDLV 176
CC	Db	124 ALCTKPPELLIRTIMGWTLDFLRRLGGIQQGWDGELL 162
CC	RESULT 14	
CC	ID	ARI1_XENLA STANDARD; PRT; 204 AA.
CC	AC	O91828;
CC	DT	01-NOV-1997 (Rel. 35, Created)
CC	DT	01-NOV-1997 (Rel. 35, Last sequence update)
CC	DT	15-JUN-2002 (Rel. 41, Last annotation update)
CC	DE	Apoptosis regulator R11 (XR11).
CC	OS	Xenopus laevis (African clawed frog).
CC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
CC	OX	Nebi_Taxid=8355;
CC	RN	[1]
CC	RP	SEQUENCE FROM N.A.
CC	RC	TISSUE=Head;
CC	RX	MEDLINE=95331613; PubMed=7607538;
CC	RA	Cruz-Reyes J., Tata J.R.;
CC	RT	"Cloning, characterization and expression of two Xenopus bcl-2-like
CC	RL	cell-survival genes.";
CC	Gene	158:171-179(1995).
CC	-1-	FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
CC	-1-	SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC	-1-	DEVELOPMENTAL STAGE: DEVELOPEMENTAL REGULATION ONLY OCCURS IN THE
CC	-1-	BRAIN OF MID-METAMORPHOSIS TO POST-METAMORPHOSIS TADPOLES AND
CC	-1-	ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC	-1-	SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC	-1-	SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC	-1-	SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC	CC	-----
CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	CC	entities requires a license agreement (See http://www.isb-sdb.ch/announce/

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CC DR EMBL; X82461; CAAS7844.1; -.
CC DR HSSP; Q07817; IMAZ.
CC DR InterPro; IPR002475; BCL2_family.
CC DR InterPro; IPR000712; Bcl2_BH.
CC DR InterPro; IPR003093; Bcl2_BH4.
CC DR InterPro; IPR004725; Bcl2_reg.
CC DR Pfam; PF00452; Bcl-2; 1.
CC DR Pfam; PF02180; BH4; 1.
CC DR SMART; SM00337; BCL; 1.
CC DR SMART; SM00265; BH4; 1.
CC DR TIGRfams; TIGR00865; bcl-2; 1.
CC DR PROSITE; PS01080; BH1; 1.
CC DR PROSITE; PS01052; BH2; 1.
CC DR PROSITE; PSS0062; BCL2_FAMILY; 1.
CC DR Apoptosis; Transmembrane.
CC KW DOMAIN 101 120 BH1.
CC FT DOMAIN 152 167 BH2.
CC FT TRANSMEM 181 198 POTENTIAL.
SQ SEQUENCE 204 AA; 23379 MW; 3BFC6BE6DDA4CA03 CRC64;

Query Match 12.6%; Score 138.5; DB 1; Length 204;
Best Local Similarity 26.2%; Pred. No. 1.9e-05;
Matches 28; Conservative 22; Mismatches 54; Indels 3; Gaps 1

QY 66 EVCTVLTLELGELQIRPSVYRNVAQLHIPLOSPPVTDAFLAVAGHIFSGITMGKV 125
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 57 EVLQALTEATEBEFELRYGRAFSDLNLSQH---TQDIAQSISQYVMGELFRGTNGRIIV 113
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 126 SLYSAAAGLVDCVQAQAPAMVHALVDLCGEFVKRTLATWLRRGW 172
   :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 114 AFGSRGALCVESANKETDILPRIVQMNVNYLETHTLPWMQENGW 160

RESULT 15
BCLX_CHICK STANDARD; PRT; 229 AA.
AC Q07816; Q98908;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-X.
GN BCL2L1 OR BCLX OR BCL-X.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (SHORT FORM).
RX MEDLINE=93364977; Pubmed=8358789;
RA Bolse L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT of apoptotic cell death."
RL Cell 74:597-608(1993).
RN [2]
RP SEQUENCE FROM N.A. (LONG FORM).
RX STRAIN=Hubbard White Mountain; TISSUE=Testis;
RX MEDLINE=97264485; Pubmed=9110311;
RA Villagrosa X., Mezquita C., Mezquita J.;
RT "differential expression of bcl-2 and bcl-x during chicken
RT spermatogenesis."
ML Mol. Reprod. Dev. 47:26-29(1997).
CC -1 FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
CC ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY)
CC -1 SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC ENVELOPE (BY SIMILARITY).
CC -1 ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1 TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
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CC DEVELOPMENT.
CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC FUNCTION. INTRACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC APOPTOTIC ACTIVITY (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z23110; CAA80657.1; -.
DR EMBL: U26645; AAB07677.1; -.
DR PIR: A47537; A47537.
DR HSSP: P53563; IAF3.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR003093; BCL2_BH4.
DR InterPro: IPR004725; BCL2_reg.
DR Pfam: PF00452; Bcl2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRfam: TIGR00865; bcl-2; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PS50063; BH4_2; 1.
DR Apoptosis: Transmembrane; Alternative splicing.
KW DOMAIN
FT DOMAIN 4 24 BH4.
FT DOMAIN 82 96 BH3.
FT DOMAIN 125 144 BH1.
FT DOMAIN 176 191 BH2.
FT TRANSMEM 206 223 POTENTIAL.
FT VARSPIC 185 229 ERFVDLYGNMAAEELRKGOETPFNKILTGATVAGVLLIGSL
SO SEQUENCE 229 AA; 25733 MW; A97D3A4D04C0E9DA CRC64;

Query Match 12.5%; Score 137.5; DB 1; Length 229;
Best Local Similarity 22.0%; Pred. No. 2.7e-05;
Matches 42; Conservative 30; Mismatches 68; Indels 51; Gaps 5;

OY 23 TDKELVQAQKALGREYVHARLLRAGLSWAPP-----RASPA---P 60
DB 4 SNRELVI-----DFVSYKLSORGHCSLEEDENRTDTAAEAEMDSVLNGSPSWHP 56
OY 61 GG-----RLAEVCTVLLRLGDELEQIRSVYRNVARQULHPILOSEP 101
DB 57 AGHYVNGATVYRRSSLEVEHYIVASDVROALRDAGDEFELRYRRASFSLTSLHT--TPG 113
OY 102 VTTDAFLAVAGHISAGITGCKVSVLSAAGLAVDCYRQAPAMVHALVDCLGEFVRKT 161
DB 114 TAYGSFEGVAVNELFPHDGVNMGRIYAFSFGALCVESVDKEMRVLYGRIVSMVTYLTLDH 173
OY 162 LATWLRRRGW 172
DB 174 LDPWIOENGW 184
```

Search completed: April 29, 2003, 11:23:56  
Job time : 8.50783 secs



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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:20:36 ; Search time 13.3473 Seconds

(without alignments)  
1534.145 Million cell updates/sec

Title: US-09-682-667-6

Perfect score: 1100

Sequence: 1 MEVLRSSVFPAEIMDAFDR.....TLCFGRFLKAFILLPER 213

Scoring table: BIOSUM62

Gapop 10.0 , Gapect 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164.5	15.0	236	2 I53744	gene bcl-2 protein
2	159.5	14.5	236	2 JC7383	B-cell lymphoma 2
3	159	14.5	236	2 I67432	BCL-2 - rat (fragm
4	158.5	14.4	227	2 JE0203	apoptosis regulato
5	157.5	14.3	236	1 TVMSA1	transforming prote
6	156	14.2	216	2 B37332	transforming prote
7	155	14.1	233	2 A37332	transforming prote
8	153.5	14.0	239	1 TVHUA1	transforming prote
9	151.5	13.8	232	2 S24390	transforming prote
10	150.5	13.7	199	1 TVMSB1	transforming prote
11	150.5	13.7	214	2 I49057	bcl-x transmembran
12	150.5	13.7	233	2 I49056	bcl-x long - mouse
13	149.5	13.6	233	2 S51761	BCL-X protein - ra
14	148.5	13.5	218	2 B47538	BCL-2-associated p
15	148	13.5	233	2 I67431	BCL-X-long - rat
16	146.5	13.3	233	2 B47537	apoptosis regulato
17	145.5	13.2	179	2 JC7255	Bax-delta protein
18	145.5	13.2	205	1 TVHUB1	transforming prote
19	143.5	13.0	192	2 A47538	bcl-2-associated p
20	137.5	12.5	190	2 A47537	apoptosis regulato
21	127.5	11.6	192	2 D47538	bcl-2-associated p
22	127.5	11.6	211	2 S58873	Bak protein - huma
23	123	11.2	133	2 I53293	bcl-2-associated p
24	122.5	11.1	211	2 S58875	cdn-2 protein - hu
25	120	10.9	350	2 A47476	BCL2 homolog MCL1
26	110.5	10.0	143	2 I38921	bcl-2-associated p
27	105	9.5	154	2 I58194	gene bcl-2 protein
28	97.5	8.9	115	2 A70990	carbamoyl-phosphat
29	95.5	8.7	172	2 I49449	hemopoietic-specif

30	94.5	8.6	1203	2 I55466	N-methyl-D-asparta
31	92	8.4	860	2 C82750	mannosyltransferas
32	91.5	8.3	175	2 I39055	Bcl-2 related - hu
33	90.5	8.2	118	2 S70089	KorA protein - Amy
34	89	8.1	411	2 E70667	hypothetical prote
35	88.5	8.0	1129	2 H86975	probable carbamoyl
36	87	7.9	373	2 H84404	ferrichrome ABC tr
37	85.5	7.8	600	2 D87232	conserved membrane
38	85	7.7	552	2 S71811	probable transcrip
39	83	7.5	177	2 S54778	NR-13 protein - qu
40	82.5	7.5	255	2 JC7567	cardamoyl-phosphat
41	82.5	7.5	1105	2 S76557	transcription regu
42	82	7.5	300	2 AC1088	syngomyacin synth
43	82	7.5	9376	2 T14593	3-deoxy-D-manno-oc
44	81.5	7.4	416	2 E87286	probable membrane
45	81	7.4	591	2 T44868	

## ALIGNMENTS

## RESULT 1

I53744 gene bcl-2 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 16-Jul-1999

C:Accession: I53744

R:Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.

Gene 140, 291-292, 1994

A>Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.

A:Reference number: I53744; M0ID:94193015; PMID:8144041

A:Accession: I53744

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-236 <RES>

A:Cross-References: GB:I14680; NID:q408946; PIDN:AAAS3662.1; PID:q408947

C:Gene(s):

A:Gene: bcl-2

C:Superfamily: bcl transforming protein

Query Match 15.0%; Score 164.5; DB 2; Length 236;

Best Local Similarity 23.3%; Pred. No. 1.4e-07;

Matches 52; Conservative 35; Mismatches 79; Indels 57; Gaps 8;

QY 28 VQAOKALG-----REYVHARLRLAGLSW-----SAPRASAPAP-----61

DB 1 MAQAGRTGYDNREIVMKYIHKLSQKGYEMDGDDEDSAPLRAAPYQIFSFQFESNRTPA 60

QY 62 -----GRLAEVCTVLRIGLDELQIRPSVYRNVAR-----QLHI-P 96

DB 61 VHRDTAARTSPRLPPLVANAGPALSPVPVYHLTLRRAGDDFSRRYRDFAEMSSQLHLTP 120

QY 97 LQSEPVYTDLFLAVAGIIFAGITGWKVSLSYSAAGLAVDCYRQAPAVVHLLVDCIGE 156

DB 121 FTRAR---GRTAVVELEFLDGVNMGRIVAFFEGGVGCVSNREMSPLVDNALMTE 176

QY 157 FVAKTLATLRRRGQWTDVLCV-VSPKPGFRHML-VATLCS 197

DB 177 YLNRHLHTWTQDNGMDAFVFLYGPSPRLPFDLSWLKTLLS 219

## RESULT 2

JC7383 B-cell lymphoma 2 protein - Chinese hamster

C:Species: Cricetus griseus (Chinese hamster)

C>Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 08-Dec-2000

C:Accession: JC7383

R:Tomlicic, M.T.; Christmann, M.; Kalna, B.

Biochem. Biophys. Res. Commun. 275, 899-903, 2000

A>Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.

A:Reference number: JC7383

A:Contents: Ovary

A:Accession: JC7383

A: Molecule type: mRNA  
A: Residues: 1-236 <TOM>  
A: Cross-references: GB:AJ271720  
C: Comment: This protein has anti-apoptotic function, and supports cell survival.  
C: Genetics:  
A: Gene: bcl-2  
C: Superfamily: bcl transforming protein  
C: Keywords: B-cell lymphoma; ovary

Query Match	14.5%	Score 159.5	DB 2	Length 236
Best Local Similarity	22.4%	Pred NO. 4e-07		
Matches 50; Conservative	37;	Mismatches 79;	Indels 57;	Gaps 8

```
OY      28 VAOAAALG-----REVHARLLRAGISW-----SAPERASAPC-----61
Db      1 MAQAGRITGYDNREIYMKTIHKLSRGXYEMDGVDAAPLGAATPPEITSFQESNPTPA 60
OY      62 -----GLAEVCYVLLRLGDELEQIRPSYRVNR-----OLHI-P 96
Db      61 VHRDMAATSPLRPRIIVATTGPILLSPPVPVVHLTLRRAGDDFSRRYRRDPAMSSQLHTLP 120
OY      97 LOSEPVVTDAFLAVAGHTFFSGITGWKYVSILYSAAGLAVDCYRQAOPANVAHALVDPCLGE 156
Db      121 FTAR----GRATVAVEELFRDGVNMWRIGIAVFEEFGYGVACVESYVRKMSPLVDNIAlMTE 176
OY      157 FVKRTIATVLRRRGGWMDVLKC-VSTRKPGSRHWL-VATLCS 197
Db      177 YLNRLHATWIODNGMDAFAVELYPSPVRAPLRDFESWLTKLTLLS 219
```

RESULT 3  
I67432

BCL-2 - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Jul-1999  
 C:Accession: I67432  
 R:Title: J.L.; Tilly, K.I.; Kerton, M.L.; Johnson, A.L.  
 Endocrinology 136, 232-241, 1995  
 A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: constitutive bcl-2 and bcl-x long messenger ribonucleic acid levels.  
 A:Reference number: 153295; MUID:95129487; PMID:7828536  
 A:Accession: 167432  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-236 <RES>  
 A:Cross-references: EMBL:U34964; NID:g1004378; PIDN:AA77687.1; PID:g1004379  
 C:Superfamily: bcl transforming protein

Query Match	14.58	Score	159;	DB 2;	Length	236;			
Best Local Similarity	21.58	Pred	No. 4.4e-07;						
Matches	51;	Conservative	37;	Mismatches	83;	Indels	66;	Gaps	8

```

OY 28 VAAKKAAG-----REVHARLLRAGISW-----SAPRASAPAP-----61
Db 1 MAQAGRGYDKNRELKYMKIHKILKSORGYEMTDGEDSAPLRAPTPGIFSPESNRTPA 60
OY 62 -----GRLEAVCTVLLRLGDELQIRPSYRNAR-----OLHI-P 96
Db 61 VHRDTAATSPLRPLRNAGPALSPVPPVHLLTRAGDDFSRRYRDRFAMSSQHLTP 120
OY 97 LQSEPVYTDALAVAGHIFSGITGWKRVSLYSAAAGLAVDCYRQAPANVHALVDCGE 156
Db 121 FTAR-----GRATVVEELFRDGVNMGRIVAFFEEFGYGVESVNRREMYPLVDNIATMTE 176
OY 157 FVRKTLATLERRRGWMTDYLKCV-VSRKPGGRSHW-----IVATLCSGRRL 202
Db 177 YLNRHLHTWIDONGMAPEVELGSPSRMLPDRDFSWOSLKTLLSLALVAGACTTIGATL 233

```

RESULT 4  
JE0203  
Apoptosis regulator bcl-x isoform - human  
N;Alternate names: h-bcl-xbeta

C:Species: Homo sapiens (man)  
C:Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 16-Jul-1999  
C:Accession: JE00203  
R:Ban, J.; Echatt, L.; Wengler, W.; Wildner, M.; Tschachler, E.  
Biochem. Biophys. Res. Commun. 248, 147-152, 1998  
A:Title: Identification of a human cDNA encoding a novel bcl-x isoform.  
#:Reference number: JE00203; MID:98340865; PMID:9675101

Query Match	14.48	Score 158.5	DB 2	Length 227
Best Local Similarity	23.58	Pred. No. 4.7e-07		
Matches 50	Conservative 29	Mismatches 77	Indels 57	Gaps 6

```

QY 23 TDKELVQAQAKKAGREYVHARLLRAGLSMS-----APEKA-----56
Db 4 SNRELIV-----DFLSYKLSQKGYSQPSQDVEENRTEAPBCTESEMETPSAINGNPS 56
QY 57 -----SPAGGR-----LAEYCTVLLRLGDELEQIRPSVRYNRVAQOLHPL 97
Db 57 WHLADSPRVNATGHSSSLDAREVYIPMAAVYQALRENGDEBELRYRRAFSDLSQHLI-- 114
QY 98 QSEPVYTDALFVAGHIFPSAGITWKKVSLYSAAGLAVDCVROAPAMVHALVDCGEF 157
Db 115 -TPGTAAYOSEQVYNNELFRRDGVNMGRIYAFESFGALCVESVDKEMOVLSTRANMAYV 173
QY 158 VRKTLATWLRRRGM--TDVLKCVYVSTPKPRRS 188
Db 174 LNDHLEPWIOENGWVRKPELVCPFSIASGORS 206

```

## RESULT 5

transforming protein bcl-2-alpha - mouse  
 TVMSAI  
 C:Species: Mus musculus (house mouse)  
 C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 18-Jun-1999  
 C:Accession: A25960; E37332  
 R:Negritini, M.; Siliini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.  
 Cell 49, 455-463, 1987  
 A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene  
 A:Reference number: A90893; MUID:87187643; PMID:3032455  
 A:Accession: A25960  
 A:Molecule type: DNA  
 A:Residues: 1-236 <NEC>  
 A:Cross-references: GB:L11532; GB:M16506; NID:q468336; PIDN:AA37282.1; PID:g387109  
 R:Guch, Y.; Ewert, D.L.; Tsujimoto, Y.  
 Nucleic Acids Res. 20, 4187-4192, 1992  
 A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a va  
 A:Reference number: A37332; MUID:92375724; PMID:1508712

A: Introns: 192/3  
C: Superfamily: bcl transforming protein  
Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane

Query Match            14.3%   Score 157.5; DB 1; Length 236;  
Best Local Similarity   22.4%; Pred. No. 6e-07; Mismatches 57; Gaps 8;  
Matches     50; Conservative     37; Indels       57;

OY      28 VQAQALG-----REYVHARLLTRAGLSM-----SAPERASAPAG----- 61  
||| | :|: | :| |  
Db    1 MAQAERTGDNREIYMKYTHRYKLSQRGEWMDAGDADAAPLGAAPTGLTSPDESMPMA 60

```
QY      62 -----GRLAECVTVLLRLGDEIQIPSYRNNAR-----TOLHI-P   96  
         |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
Db      61 VHREMAATSPRLPLVTAGALSPVPCCVHLTLRRAGDDFSRRRYRDFAEMSSQLTP    120  
  
QY      97 LQSEPVTTDAFLAAGHIFSGITWGVKVSLSYSAAGAIVDCVQAQPAUWHALVDCTGE   156  
         |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
Db     121 FTAR----GREAYVEELFRDGVNMGRIYAFEEGGVMCVESVNREMSPLVDNALMTE   176  
  
QY     157 FVRKTLATWLRRRGMTDVLCKV-VSRKPFRSHML-VATLCS   197  
         ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
Db     177 YLNRLHTWIODNGMDAPFELYLPSPKRPLFDPSWLSLKLTLLS   219
```

RESULT 6  
B37332  
transforming protein (bcl-2-beta) - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 24-Apr-1998  
C:Accession: B37332; S35452  
R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992  
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues  
A:Reference number: A37332; MUID:92375724; PMID:1508712  
A:Accession: B37332  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-216 <ESCU>  
A:Cross-references: EMBL:DJ1381; EMBL:DJ1382  
C:Superfamily: bcl transforming protein

RESULT 7

A37332

transforming protein (bcl-2-alpha) - chicken

C:Species: Gallus gallus (chicken)

C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 23-Feb-1997

C:Accession: A37332; S35453

R:Equgchl, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues

A:Reference number: A37332; MUID:92375724; PMID:1508712

A:Accession: A37332

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-233 <EGU>

A:Cross-references: EMBL:DL1381

C:Genetics:

A:Introns: 189/3

C:Superfamily: bcl transforming protein

C:Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 14.1%; Score 155; DB 2; Length 233;

Best Local Similarity 20.6%; Pred. No. 1e-06;

	Matches	45;	Conservative	36;	Mismatches	81;	Indels	56;	Gaps	6;
QY	37	EYVHARLLRAGLSMSA-----	PERASPAQGLAEVCT-----							69
		: : : : :	: : : : :							
Db	17	KYIHKYLISQRYDVAAGEDRPVPAPAPAAAPAAVAAAGASSHHRRPEPGSAAASEVPP								76
		: : : : :	: : : : :							
QY	70	-----VLLRIGDELEQTRPSPVRYNVARQLH-PLQSEPVYDALTLVAAGHIF								115
		: : : : :	: : : : :							
Db	77	AEGLRPAPPGYHLLARQAGDEFSRRYQDFAFQMSQLHPTTAH-----GRVAVAYEELEF								132
		: : : : :	: : : : :							
QY	116	SAGITGKGVVSLYSAAAGLAIVDCVRAQAPFAMVHALVDCIEGFVVKTLATLRRRGQMTDV								175
		: : : : :	: : : : :							
Db	133	RDGVNMGRIVAFPEFEGGVYCVESVYREMSPLVDNATMTATEYLNRHNLHMIDONGMDAF								192
		: : : : :	: : : : :							
QY	176	LKCV-VSTKPGFRSHW-----	LVAATCSFGRFL							202
		: : : : :	: : : : :							
Db	193	VELYGNSMRPLDFDSWISLKTLLSLVYLGAACITLCAVTL								230

RESULT 8

TVHNA1

transforming protein bcl-2, splice form alpha - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1998 #sequence revision 07-Jun-1996 #text-change 15-Oct-1999

C:Accession: G37332; A29409; S02452; A24428; A27622; B27622

R:Equchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a v

A:Reference number: A37332; MUID:92375724; PMID:1508712

A:Accession: G37332

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-239 <FCU>

A>Note: this report is a correction

R:Tsujimoto, Y.; Croce, C.M.

Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986

A:Title: Analysis of the structure, transcripts, and protein products of bcl-2, the

A:Reference number: A29409; MUID:86259760; PMID:3523487

A:Accession: A29409

A:Molecule type: mRNA

A:Residues: 1-95, 'A', 97-109, 'G', 111-236, 'S', 238-239 <TSU>

A:Cross-references: GB:M1394; NID:g179366; PIDN:AAA51813.1; PID:g179367

A>Note: this sequence has been corrected in reference A37332.

R:Seio, M.; Jaeger, U.; Hockett, R.D.; Gruninger, W.; Bennett, S.; Goldman, P.; Kors

EMBO J. 7, 123-131, 1988

A:Title: Alternative promoters and exons, somatic mutation and deregulation of the B

A:Reference number: S02452; MUID:88196071; PMID:2834197

A:Accession: S02452

A:Molecule type: mRNA

A:Residues: 1-239 <SEP>

R:Cleary, M.L.; Smith, S.D.; Sklar, J.

Cell 47, 19-28, 1986

A:Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immun

A:Reference number: A24428; MUID:87002488; PMID:2875799

A:Accession: A24428

A:Molecule type: mRNA

A:Residues: 1-58, 'T', 60-116, 'R', 118-239 <LE>

A:Cross-references: GB:M4745; NID:g179370; PIDN:AAA5591.1; PID:g179371

R:Hu, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakhshi,

Oncogene Res. 2, 263-275, 1988

A:Title: Consequences of the t(14;18) chromosomal translocation in follicular lympho

A:Reference number: A27622; MUID:86217344; PMID:3285301

A:Accession: A27622

A:Molecule type: mRNA

A:Residues: 1-58, 'T', 60-239 <HUA>

A:Accession: B27622

A:Molecule type: DNA

A:Residues: 1-6, 'S', 8-58, 'T', 60-128, 'C', 130-239 <HUA>

A>Note: the sequence was determined from the germline gene

C:Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocat

C:Genetics:

A:Gene: GDB:BCL2

A:Cross-references: GDB:119031; OMTM:151430

A:Map position: 18q21.3-18q21.3

C:Function:

A:Description: blocks apoptosis in hematopoietic cells

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match 14.0%; Score 153.5; DB 1; Length 239;

Best Local Similarity 21.9%; Pred. No. 1.4e-06;

Matches 46; Conservative 37; Mismatches 74; Indels 53; Gaps 7;

QY 37 EYVHARLLRAGLSW-----SAPERASAPAG-----GRLAEVCT-- 69

DB 17 KYIHXYLSQRYEMDAGDCAAPGAPAGGINSQPGHTPHPAASNDPVARFSPLOTPTA 76

QY 70 -----VLLRLGDELEQIRSVYRNVAROLHLP-LOSEPVVTDALFLA 109

DB 77 APCAAGAPALSPVPVYHLLTRQAGDDEFSRRYRDRFAEMSSQLHLPFTAR---GREAT 132

QY 110 VAGHIFASGITWGVSLYSAAGLAVDCVROAPAMVHALVDCLEGFVKTLATMLRR 169

DB 133 VVEELFPRDGVNMGRIYAFEFEGVCMCVESYNREMSPLVDNIALMTEYLRHLHTWIQDN 192

QY 170 GGWTDVLKCV-VSTKPGFRSHML-VATLCS 197

DB 193 GGWDAFVELYGFPSMRPLDFFSWLSLTKLTS 222

RESULT 9

S24390

transforming protein (Bcl-2) homolog - chicken

C:Species: Gallus gallus (chicken)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999

C:Accession: S24390

R:Caazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.

Biochim. Biophys. Acta 1132, 109-113, 1992

A:Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue

A:Reference number: S24390; MUID:92379084; PMID:1511008

A:Accession: S24390

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-232 <CAZ>

A:Cross-references: EMBL:211961; NID:962969; PIDN:CAA78018.1; PID:962970

C:Superfamily: bcl transforming protein

C:Keywords: mitochondrion; transmembrane protein

Query Match 13.8%; Score 151.5; DB 2; Length 232;

Best Local Similarity 20.4%; Pred. No. 2.1e-06;

Matches 44; Conservative 36; Mismatches 83; Indels 53; Gaps 5;

QY 37 EYVHARLLRAGLSWSA-----PERASAPAGRLAEVCT----- 69

DB 17 KYIHXYLSQRYEMDAGDCAAPGAPAGGINSQPGHTPHPAASNDPVARFSPLOTPTA 76

QY 70 -----VLLRLGDELEQIRSVYRNVAROLHLP-LOSEPVVTDALFLA 117

DB 77 LRGCAAPGCVHLLRQAGDEFSRRYRDRFAEMSSQLHLP---TPFATGRFAVVEELFND 133

QY 118 GITWGVSLYSAAGLAVDCVROAPAMVHALVDCLEGFVKTLATMLRRGGWTDVLK 177

DB 134 GVNWRIVAFEEFGVCMCVESYNREMSPLVDNIALMTEYLRHLHTWIQDN 193

QY 178 CV-VSTKPGFRSHW-----LVATLCSFGRF 202

DB 194 LVGNSMRPLDFFSWLSLTKLTSVLVYGACITIGATL 229

RESULT 10

transforming protein bcl-2-beta - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 18-Jun-1999

C:Accession: B25960

R:Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.

Cell 49, 455-463, 1987

A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene ho

A:Reference number: A90893; MUID:87187643; PMID:3032455

A:Accession: B25960

A:Molecule type: DNA

A:Residues: 1-199 <NEG>

A:Cross-references: GB:M16506; NID:9468335; PIDN:AAA37281.1; PID:9387110

C:Genetics:

A:Gene: BCL2

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; transforming protein

Query Match 13.7%; Score 150.5; DB 1; Length 199;

Best Local Similarity 22.1%; Pred. No. 2.2e-06;

Matches 45; Conservative 34; Mismatches 68; Indels 57; Gaps 7;

QY 28 VAOAKALG-----REYHARLLRAGLSW-----SAPERASAPAG----- 61

DB 1 MAQAGRTGYNREIVTKYIKLSQRYEMDAGDADADAPLGAAPTFEISFOEPSNMPA 60

QY 62 -----GRLAEVCTVLLRLGDELEQIRSVYRNVAR-----QLHI-P 96

DB 61 VREMAARTSPLRPLVATAGPALSVPVPCVHLLTRAGDDEFSRRYRDRFAEMSSQLHLP 120

QY 97 LOSEPVTDAFLAVAGHIFASGITWGVSLYSAAGLAVDCVROAPAMVHALVDCLEG 156

DB 121 FTAR---GREATVVEELFPRDGVNMGRIYAFEFEGVCMCVESYNREMSPLVDNIALMTE 176

QY 157 EVRKTATWLRRRGWTDVLKCV 180

DB 177 YLNRHLHTWIQDNQGW-VGACLV 198

RESULT 11

149057

bcl-x transmembrane deleted - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999

C:Accession: I49057

R:Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.

J. Immunol. 153, 4388-4398, 1994

A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes

A:Reference number: I49055; MUID:95052604; PMID:7963517

A:Accession: I49057

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-214 <RES>

A:Cross-references: EMBL:U10102; NID:9506649; PIDN:AAA82174.1; PID:9506650

C:Genetics:

A:Gene: bcl-x-long

C:Superfamily: bcl transforming protein

Query Match 13.7%; Score 150.5; DB 2; Length 214;

Best Local Similarity 22.1%; Pred. No. 2.4e-06;

Matches 43; Conservative 29; Mismatches 68; Indels 55; Gaps 5;

QY 23 TKEVLAQKALGREYHARLLRAGLSWS-----ADPRA----- 56

DB 4 SNRELIV-----DFLSYLSQKGYMSQFSDEENRTAEDETEAERETPSAINGNS 56

QY 57 -----SPARGGR-----LAECVYLLRLGDELEQIRSVYRNVAROLHLP 97

DB 57 WHLAOSPANAGATGSHSSIDAREVEMAVKQALREAGDEFEIRRRARRASDLSOLHI-- 114

QY 98 OSEPVTDAFLAVAGHIFASGITWGVSLYSAAGLAVDCVROAPAMVHALVDCLEG 157

DB 115 -TPGTAQVSFEQVVELFNDGVNMGRIYAFEFEGALCVESDKENQVLYSRIASMATY 173

QY 158 VKRTLATWLRRRGW 172

DB 174 LNDHLEPWIQENGW 188



A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-233 <RES>  
A:Cross-references: EMBL:U34963; NID:q1004376; PID:AAA7686.1; PID:q1004377  
C:Superfamily: bcl transforming protein

Query Match 13.5%; Score 148; DB 2; Length 233;  
Best Local Similarity 22.4%; Pred. No. 4.4e-06;  
Matches 53; Conservative 33; Mismatches 89; Indels 62; Gaps 7;

```
OY 23 TDKEIYAQAKALGREYVHARLLRAGLSWS-----APER----- 56
   |||
DB 4 SNRELIV-----DPLSKLSQKGYSMQSFSDVEENRTAEPEPEPEPEPSAINGNPS 56
   |||
OY 57 -----SPAGGR-----LAECVTLRLGDELEQIRPSVYRNVARQLHPL 97
   |||
DB 57 WLIADSPAVNGATGSSSIDAREVLPMAAVKQALREAGDEFELRYRAFSDLTSQLHI-- 114
   |||
OY 98 OSEPVYDAFLAVAGHITSAGITNGKRVSLYSAAGLAVDCYRQAPAMVHALVDCIGEE 157
   |||
DB 115 -TPGTVYOSFEQVNELEFRDGVNMGRIYASSSEFGALCVESYDKEMOVLVSRIASMMATY 173
   |||
OY 158 VRKTLATWLRRCGW-TDVLKCVSTKPGFR-----SHLVATLCSFGRLKAAFF 207
   |||
DB 174 LNDHLEPMIQENGMDTVDLYGNNTAFESRKGQERFNRMLTGMTVAGVLLGSLF 230
```

Search completed: April 29, 2003, 11:26:36  
Job time : 14.3473 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:16:46 : Search time 32.5339 Seconds  
(without alignments)  
872.393 Million cell updates/sec

Title: US-09-682-667-6  
Perfect score: 1100  
Sequence: 1 MEVLRRSSVFSAEIMDAFDR.....TLCSFGRLKAFLLPER 213

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq\_101002:\*

- 1: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:\*
- 2: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*
- 3: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:\*
- 4: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:\*
- 5: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:\*
- 6: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:\*
- 7: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:\*
- 8: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:\*
- 9: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:\*
- 10: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:\*
- 11: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:\*
- 12: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:\*
- 13: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:\*
- 14: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:\*
- 15: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:\*
- 16: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:\*
- 17: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:\*
- 18: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:\*
- 19: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:\*
- 20: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:\*
- 21: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*
- 22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*
- 23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1100	100.0	213	AAV14155	Human Bcl protein
2	1076	97.8	213	AAV14153	Rat Bcl protein se
3	1055	95.9	213	AAV14144	Human ORF1208
4	852.5	77.5	170	AAV14156	Human Bcl protein
5	821.5	74.7	170	AAV14154	Rat Bcl protein se
6	716	65.1	176	AAV14154	Breast and ovarian
7	660	60.0	134	AAV14154	Human Bcl-2-like p
8	240.5	21.9	846	AAV14154	Drosophila melanog
9	230	20.9	247	AAV14154	Drosophila melanog
10	159.5	14.5	239	AAV14154	Human BCL-2 protei

11	159.5	14.5	239	22	AAV14155
12	158	14.4	232	17	AAV14155
13	158	14.4	232	20	AAV14155
14	157.5	14.3	236	20	AAV14155
15	157.5	14.3	236	20	AAV14155
16	157.5	14.3	236	22	AAV14155
17	157.5	14.3	236	23	AAV14155
18	157.5	14.3	236	22	AAV14155
19	156.5	14.2	272	17	AAV14155
20	155.5	14.1	239	17	AAV14155
21	155.5	14.1	239	22	AAV14155
22	155.5	14.1	239	22	AAV14155
23	155	14.1	239	19	AAV14155
24	155	14.1	239	21	AAV14155
25	155	14.1	485	22	AAV14155
26	154.5	14.0	239	9	AAV14155
27	154.5	14.0	239	14	AAV14155
28	154.5	14.0	239	16	AAV14155
29	154.5	14.0	239	16	AAV14155
30	154.5	14.0	239	17	AAV14155
31	154.5	14.0	239	19	AAV14155
32	154.5	14.0	239	20	AAV14155
33	154.5	14.0	239	20	AAV14155
34	154.5	14.0	239	22	AAV14155
35	154.5	14.0	239	22	AAV14155
36	154.5	14.0	239	22	AAV14155
37	154.5	14.0	239	23	AAV14155
38	154.5	14.0	239	23	AAV14155
39	153.5	14.0	239	20	AAV14155
40	153.5	14.0	239	22	AAV14155
41	153.5	14.0	239	22	AAV14155
42	153.5	14.0	239	23	AAV14155
43	152.5	13.9	229	17	AAV14155
44	152.5	13.9	229	20	AAV14155
45	152.5	13.9	239	22	AAV14155

## ALIGNMENTS

RESULT 1	
AAV14155	AAV14155 standard; Protein; 213 AA.
XX	
AC	AAV14155;
XX	
DT	27-JUL-1999 (first entry)
XX	
DE	Human Bcl protein sequence.
XX	
KW	Bcl protein; Bcl-2-related ovarian killer; BH3 variant; endometrial; pro-apoptotic protein; apoptosis inducer; hyperproliferation disease; reproductive tissue; uterine carcinoma; testicular carcinoma; cervix; ovarian carcinoma; granulosa epithelial carcinoma; cancer; therapy;
KW	proliferative disorder; human.
OS	Homo sapiens.
XX	
PN	W09924453-A1.
XX	
PD	20-MAY-1999.
XX	
PF	04-NOV-1998; 98WO-US23523.
XX	
PR	07-NOV-1997; 97US-0064943.
XX	
PA	(STRD ) UNIV LELAND STANFORD JUNIOR.
XX	
PI	Hsu SY, Hsueh AWJ;
XX	
DR	WPI: 1999-327356/27.
XX	
DR	N-PSDB; AAV1105.
XX	

PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
 PT protein and its related gene

PS Claim 2; Page 55-56; 62pp; English.

CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
 CC protein, of the invention. Coding sequences for Bok or Bhl3 variants of  
 CC pro-apoptotic Bok-related protein can be introduced into cell populations  
 CC to upregulate expression of the proteins in order to induce apoptosis in  
 CC the cell population. This is useful for treatment of diseases where there  
 CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
 CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
 CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
 CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
 CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
 CC other tissues, and provide a means for manipulating apoptosis. The Bok  
 CC protein and transgenic animal are also useful for identifying ligands or  
 CC substrates. Modulation of the gene activity in vivo is useful for  
 CC prophylaxis and therapy of, e.g. cancer and other proliferative  
 CC disorders. Bok genes are also useful for identification of cell type  
 CC based on expression. Identification of Bok as a new pro-apoptotic protein  
 CC with wide tissue distribution and heterodimerisation properties  
 CC facilitates elucidation of apoptosis mechanisms.

XX Sequence 213 AA:

SO Query Match 100.0%; Score 1100; DB 20; Length 213;

Best Local Similarity 100.0%; Pred. No. 3.6e-112;  
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEVLRSSVFPAEIMDADRPMTDKELVAQAKALGREYVHARLLRAGLSMSAPERASAP 60  
 DB 1 MEVLRSSVFPAEIMDADRPMTDKELVAQAKALGREYVHARLLRAGLSMSAPERASAP 60  
 OY 61 GGRLAEVCTVLLRLGDELEQIRPSYRNVARQLHPILOSEPVYDAFLAVAGHIFSAGIT 120  
 DB 61 GGRLAEVCTVLLRLGDELEQIRPSYRNVARQLHPILOSEPVYDAFLAVAGHIFSAGIT 120  
 OY 121 WGVVSLYSAAGLAVDCVROAOPAMVHALVDCGEEFVRKTLATWLRRRGSGMTDVLKCV 180  
 DB 121 WGVVSLYSAAGLAVDCVROAOPAMVHALVDCGEEFVRKTLATWLRRRGSGMTDVLKCV 180  
 OY 181 STKPGFRSHMLVATLCSFGRFKAAFFILLPER 213  
 DB 181 STKPGFRSHMLVATLCSFGRFKAAFFILLPER 213

RESULT 2  
 ID AAY14153 standard; Protein: 213 AA.

XX AAY14153;

DT 27-JUL-1999 (first entry)

XX Rat Bok protein sequence.

XX Bok protein; Bcl-2-related ovarian killer; Bhl3 variant; endometriosis;  
 KW pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
 KW reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
 KW ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
 KW proliferative disorder; rat.

XX Rattus rattus.

XX MO9924453-A1.

XX 20-MAY-1999.

XX 04-NOV-1998; 98WO-US33523.

XX 07-NOV-1997; 97US-0064943.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Hsu SY, Hsueh AJW;

XX WPI: 1999-327356/27.

DR N-PSDB: AAX61103.

PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
 PT protein and its related gene

PS Claim 2; Page 53-54; 62pp; English.

CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
 CC protein, of the invention. Coding sequences for Bok or Bhl3 variants of  
 CC pro-apoptotic Bok-related protein can be introduced into cell populations  
 CC to upregulate expression of the proteins in order to induce apoptosis in  
 CC the cell population. This is useful for treatment of diseases where there  
 CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
 CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
 CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
 CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
 CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
 CC other tissues, and provide a means for manipulating apoptosis. The Bok  
 CC protein and transgenic animal are also useful for identifying ligands or  
 CC substrates. Modulation of the gene activity in vivo is useful for  
 CC prophylaxis and therapy of, e.g. cancer and other proliferative  
 CC disorders. Bok genes are also useful for identification of cell type  
 CC based on expression. Identification of Bok as a new pro-apoptotic protein  
 CC with wide tissue distribution and heterodimerisation properties  
 CC facilitates elucidation of apoptosis mechanisms.

XX Sequence 213 AA:

SO Query Match 97.8%; Score 1076; DB 20; Length 213;

Best Local Similarity 98.6%; Pred. No. 1.5e-109;  
 Matches 210; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 MEVLRSSVFPAEIMDADRPMTDKELVAQAKALGREYVHARLLRAGLSMSAPERASAP 60  
 DB 1 MEVLRSSVFPAEIMDADRPMTDKELVAQAKALGREYVHARLLRAGLSMSAPERASAP 60  
 OY 61 GGRLAEVCTVLLRLGDELEQIRPSYRNVARQLHPILOSEPVYDAFLAVAGHIFSAGIT 120  
 DB 61 GGRLAEVCTVLLRLGDELEQIRPSYRNVARQLHPILOSEPVYDAFLAVAGHIFSAGIT 120  
 OY 121 WGVVSLYSAAGLAVDCVROAOPAMVHALVDCGEEFVRKTLATWLRRRGSGMTDVLKCV 180  
 DB 121 WGVVSLYSAAGLAVDCVROAOPAMVHALVDCGEEFVRKTLATWLRRRGSGMTDVLKCV 180  
 OY 181 STKPGFRSHMLVATLCSFGRFKAAFFILLPER 213  
 DB 181 STKPGFRSHMLVATLCSFGRFKAAFFILLPER 213

RESULT 3  
 ID AAB41444 standard; Protein: 213 AA.

XX AAB41444;

DT 08-FEB-2001 (first entry)

XX Human OREFX ORF1208 polypeptide sequence SEQ ID NO:2416.

XX Human; open reading frame; OREFX; detection; cytosolic; hepatotropic;  
 KW vulnerability; antiparkinsonian; neurotropic; neuroprotective;  
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
 KW antiviral; antibacterial; antifungal; antithematic; antithyroid;  
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;





DB 61 GGRLAEECTVLLRL-----GIT 77  
QY 121 WCKVSVLSAAAGLAVDCVROAPAMVHALVDCLEFVFKTLATWLRRGWTDVLCV 180  
DB 78 WCKVSVLSAAAGLAVDCVROAPAMVHALVDCLEFVFKTLATWLRRGWTDVLCV 137  
QY 181 STKPGFRSHWLVTLCSEGRFLKAAFFLLPPER 213  
DB 138 STKPGFRSHWLVTLCSEGRFLKAAFFLLPPER 170  
RESULT 5  
AAV14154  
ID AAV14154 standard; Protein; 170 AA.  
AC AAV14154;  
XX 27-JUL-1999 (first entry)  
DE Rat Bok protein sequence.  
XX Bok protein; Bcl-2-related ovarian killer; BH31 variant; endometriosis;  
XX pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
XX reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
XX ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
XX proliferative disorder; rat.  
XX Rattus rattus.  
XX WO9924453-A1.  
XX 20-MAY-1999.  
XX 04-NOV-1998; 98WO-US23523.  
XX 07-NOV-1997; 97US-0064943.  
XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX Hsu SY, Hsueh AW;  
XX WPI; 1999-327356/27.  
XX N-PSDB; AAX61104.  
XX Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
XX protein and its related gene  
XX  
XX Claim 2; Page 54-55; 62pp; English.  
XX  
XX This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
XX protein, of the invention. Coding sequences for Bok or BH31 variants of  
XX pro-apoptotic Bok-related protein can be introduced into cell populations  
XX to upregulate expression of the proteins in order to induce apoptosis in  
XX the cell population. This is useful for treatment of diseases where there  
XX is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
XX and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
XX carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
XX by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
XX protein can be used to elucidate apoptosis mechanisms in reproductive and  
XX other tissues, and provide a means for manipulating apoptosis. The Bok  
XX protein and transgenic animal are also useful for identifying ligands or  
XX substrates. Modulation of the gene activity in vivo is useful for  
XX prophylaxis and therapy of, e.g. cancer and other proliferative  
XX disorders. Bok genes are also useful for identification of cell type  
XX based on expression. Identification of Bok as a new pro-apoptotic protein  
XX with wide tissue distribution and heterodimerisation properties  
XX facilitates elucidation of apoptosis mechanisms.  
XX  
XX Sequence 170 AA:  
XX  
XX Query Match 74.7%; Score 821.5; DB 20; Length 170;  
XX Best Local Similarity 77.9%; Pred. No. 8.5e-82;  
XX Matches 166; Conservative 0; Mismatches 4; Indels 43; Gaps 1;

QY 1 MEYLRSSVFAAEIMDAFDPEDTKELVAQAKALGREYHARILRAGLSWSAPERASPAP 60  
DB 1 MEYLRSSVFAAEIMDAFDPEDTKELVAQAKALGREYHARILRAGLSWSAPERASPAP 60  
QY 61 GGRLAEECTVLLRLGDELEQIRPSYRNVAROLHLPDLOSEPVYTAFLAVAGHISAGIT 120  
DB 61 GGRLAEECTVLLRL-----GIT 77  
QY 121 WCKVSVLSAAAGLAVDCVROAPAMVHALVDCLEFVFKTLATWLRRGWTDVLCV 180  
DB 78 WCKVSVLSAAAGLAVDCVROAPAMVHALVDCLEFVFKTLATWLRRGWTDVLCV 137  
QY 181 STKPGFRSHWLVTLCSEGRFLKAAFFLLPPER 213  
DB 138 STKPGFRSHWLVTLCSEGRFLKAAFFLLPPER 170  
RESULT 6  
AAB58949  
ID AAB58949 standard; Protein; 176 AA.  
AC AAB58949;  
XX 27-MAR-2001 (first entry)  
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 657.  
XX  
XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;  
XX neotropic; neuroprotective; antiviral; antiatherogenic; hepatotropic;  
XX antidiabetic; antiinflammatory; anticancer; vulnerary; anticonvulsant;  
XX antibacterial; antifungal; antiparasitic; cardiac; immune disorder;  
XX Addison's disease; allergy; autoimmune haemolytic anemia;  
XX autoimmune thyroiditis; diabetes mellitus; Crohn's disease;  
XX multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
XX cardiovascular disorder; wound healing; neurological disease.  
XX Homo sapiens.  
XX WO20005173-A1.  
XX 21-SEP-2000.  
XX 08-MAR-2000; 2000WO-US05881.  
XX 12-MAR-1999; 99US-0124270.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Ruben SM;  
XX WPI; 2000-611515/58.  
XX N-PSDB; AAF21852.  
XX New human breast and ovarian cancer associated gene sequences and the  
XX polypeptides encoded by these genes, useful in the prevention,  
XX treatment and diagnosis of cancer, immune disorders, cardiovascular  
XX disorders and neurological diseases -  
XX  
XX Claim 11; Page 1103; 1299pp; English.  
XX  
XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human  
XX proteins AAB58711 - AAB59128. The DNA and protein sequences are  
XX associated with breast and ovarian cancer. Included in the invention are  
XX sequences AAF22032 - AAF22040 and AAB59129 which are used in the  
XX isolation and characterisation of the DNA and protein sequences of the  
XX invention. The breast and ovarian cancer associated DNA, protein, agonist  
XX or antagonist sequences exhibit cytostatic; immunosuppressive;  
XX neotropic; neuroprotective; antiviral; antiatherogenic; hepatotropic;  
XX antidiabetic; antiinflammatory; anticancer; vulnerary; anticonvulsant;  
XX antibacterial; antifungal; antiparasitic and cardiac activity. The  
XX polynucleotide and protein sequences are used in the diagnosis of cancer,  
XX particularly breast and ovarian cancer. The nucleic acid sequences,

CC proteins, agonists and agonists may also be used in the diagnosis,  
 CC prevention and treatment of immune disorders e.g. Addison's disease,  
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,  
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid  
 CC arthritis and ulcerative colitis; cardiovascular disorders such as  
 CC myocardial ischaemias; wound healing; neurological diseases such as  
 CC cerebral anoxia and epilepsy; and infectious diseases.

XX Sequence 176 AA:

Query Match 65.1%; Score 716; DB 21; Length 176;

Best Local Similarity 88.8%; Pred. No. 3.2e-70;

Matches 143; Conservative 3; Mismatches 11; Indels 4; Gaps 2;

QY 55 RASPAAGCRLAEVCT--VLLRLGDELEQIPSYRNVARQLHPILOSEPVYTDALFVAVG 112  
 DB 18 FRSGSG--LXFEGETAVLLRLGDELEEMIRPSYRNVARQLHPILOSEPVYTDALFVAVG 75  
 QY 113 HIFSAGITWGVVSLYSAAAGLAVDCVROAOPAMVHALVDCLEFVRKTLATWLRRCGM 172  
 DB 76 HIFSAGITWGVVSLYVAAGLAVDCVROAOPAMVHALVDCLEFVRKTLATWLRRCGM 135  
 QY 173 TVLKCQVSTKPGFRSHMLVATLCSGRFLKAAFFLLPER 213  
 DB 136 TVLKCQVSTDPGLSHMLVALLCSGRFLKAAFFVLLPER 176

RESULT 7

AAB85665

ID AAB85665 standard; Protein: 134 AA.

XX AAB85665;

DT 29-OCT-2001 (first entry)

DE Human Bcl-2-like polypeptide (clone HMFHE17).

KW Bcl-2-like polypeptide; autoimmune disorder; allergy; immunomodulatory;  
 KW respiratory; cardiovascular; antidiarrhetic; immunostimulant; vaccine;  
 KW immunosuppressive; antiinflammatory; gene therapy.

OS Homo sapiens.

PN WO200157060-A1.

PD 09-AUG-2001.

PE 31-JAN-2001; 2001WO-US03080.

PR 01-FEB-2000; 2000US-0179487.

PR 07-FEB-2000; 2000US-0180697.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Duan DR, Ni J;

DR WPI; 2001-476279/51.

DR N-PSDB; AAH47021.

PT Nucleic acids encoding human Bcl-2-like polypeptides, useful for  
 PT preventing, diagnosing and/or treating -  
 PS Claim 12; Page 277-278; 2855p; English.

XX The invention provides nucleic acid molecules (NAM) encoding 4 human  
 CC Bcl-2-like polypeptides (PEP1). The NAM and PEP1 may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate Bcl-2-like polypeptides' expression. The NAM may be used  
 CC to produce the soluble Bcl-2-like polypeptides by standard recombinant  
 CC methodology. The polypeptides may also be used as antigens in the  
 CC production of antibodies against Bcl-2 and in assays to identify  
 CC modulators of Bcl-2 expression and activity. The anti-Bcl-2 antibodies  
 CC and antagonists may be used to down regulate expression and activity.

CC The anti-PEP1 antibodies may also be used as diagnostic agents for  
 CC detecting the presence of Bcl-2 polyps in samples (e.g. by enzyme linked  
 CC immunosorbent assay (ELISA)). Disorders that may be prevented, diagnosed  
 CC and/or treated by the above methods include: immunodeficiencies (e.g.  
 CC a gammaglobulinemia and B cell lymphoproliferative disorder), autoimmune  
 CC disorders (e.g. rheumatoid arthritis and Grave's disease), allergic  
 CC reactions, inflammations, respiratory diseases and cardiovascular  
 CC disorders (a full list of disorders is given in the specification). The  
 CC present sequence represents a human Bcl-2-like polypeptide.

XX Sequence 134 AA:

Query Match 60.0%; Score 660; DB 22; Length 134;

Best Local Similarity 94.7%; Pred. No. 3.1e-64;

Matches 126; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 81 IRPSYRNVARQLHPILOSEPVYTDALFVAVGHIFSAGITWGVVSLYSAAAGLAVDCVR 140  
 DB 2 IRPSYRNVARQLHPILOSEPVYTDALFVAVGHIFSAGITWGVVSLYVAAGLAVDCVR 61  
 QY 141 QAOPAMVHALVDCLEFVRKTLATWLRRCGMDVLKCVSTKPGFRSHMLVATLCSFGR 200  
 DB 62 QAOPAMVHALVDCLEFVRKTLATWLRRCGMDVLKCVSTDPGLRSHMLVALLCSFGR 121  
 QY 201 FLKAAFFVLLPER 213  
 DB 122 FLKAAFFVLLPER 134

RESULT 8

AAB64401

ID AAB64401 standard; Protein: 846 AA.

XX AAB64401;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 19995.

KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PE 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE ) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI; 2001-656860/75.

DR N-PSDB; ABL08504.

PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PS interactions -

PS Disclosure: SEQ ID NO 19995; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins

CC (ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
CC  
XX  
SQ Sequence 846 AA;  
Query Match 21.9%; Score 240.5; DB 22; Length 846;  
Best Local Similarity 35.3%; Pred. No. 2.8e-17;  
Matches 55; Conservative 27; Mismatches 65; Indels 9; Gaps 4;  
QY 26 ELVAQAKALGREYVHARLLRAG--LSMSAPER----ASPARGRLEAVCYVLLRLGDEL 80  
DB 96 DIIINGKCLGQYIRRLRRAGVLRNKKYTORLNLIDPESSHVVEFPALSMGEELER 155  
QY 81 IRPSYRVNAROL-HIP--LQSEPVYTDAPLAVAGHIFSAGITGKVSLXSAAAGLAV 136  
DB 156 MHPRYTNTSRLSRPFCELESDMAPMLNLVAKDLFRSSITGKIIISIFAVCGGFAI 215  
QY 137 DCVROAQPAMVHALVDCIGEFYRKTLATVLRRCGW 172  
DB 216 DCVROGHEDYLOCLIDGLAEIIEDLVYWLINGGW 251  
RESULT 9  
ABB63760  
ID ABB63760 standard; Protein: 247 AA.  
XX  
AC ABB63760;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster polypeptide SEQ ID NO 18072.  
XX  
KM Drosophila; developmental biology; cell signalling; insecticide;  
XX  
KW pharmaceutical.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US09231.  
XX  
PR 23-MAR-2000; 2000US-191637P.  
XX  
PR 11-JUL-2000; 2000US-0614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
DR WPI; 2001-656860/75.  
XX  
DR N-PSDB; ABL07863.  
XX  
PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -  
XX  
PS Disclosure; SEQ ID NO 18072; 21pp + sequence listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
CC sequences (AB101840-AB16175) and the encoded proteins  
CC (ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX

SQ Sequence 247 AA;  
Query Match 20.9%; Score 230; DB 22; Length 247;  
Best Local Similarity 33.3%; Pred. No. 8.2e-17;  
Matches 54; Conservative 28; Mismatches 62; Indels 18; Gaps 4;  
QY 25 KELVAQAKALGREYVHARLLRAGL--SMSAPERAPAPG---GRLEAVCYVLLRLGDEL 78  
DB 87 ODIIISGRCICGHYIKRRLRSGLFNKKLGIRISIIISTSMGIVRVFPVAVYLGDEL 146  
QY 79 EDIRPSYRVNAROL-----HIPQSEPVYTDAPLAVAGHIFSAGITGKVSLXS 130  
DB 147 ERMHPRITNGVARQICRNDEGFEHFP---DAVSLLGAVGRELFRVETITMSKVISLFAI 202  
QY 131 AAGLAVDCVROAQPAMVHALVDCIGEFYRKTLATVLRRCGW 172  
DB 203 AGLSVDCVROGHPEFLPRLMESVEVIEDLVPMINENGW 244  
RESULT 10  
AAB48288  
ID AAB48288 standard; Protein: 239 AA.  
XX  
AC AAB48288;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Human BCL-2 protein.  
XX  
KM S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;  
KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;  
KM Bad; Bcl-2; tumour; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO200075184-A1.  
XX  
PD 14-DEC-2000.  
XX  
PF 05-JUN-2000; 2000WO-US15449.  
XX  
PR 04-JUN-1999; 99US-0137494.  
XX  
PA (UYIA ) UNIV YALE.  
XX  
PI Zhang H, Tsvetkov IM, Kondo T;  
XX  
DR WPI; 2001-061703/07.  
XX  
DR N-PSDB; AAC84600.  
XX  
PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,  
PT involves altering levels of proteins such as S-phase kinase associated  
PT proteins 1, 2 and cullin/CDC53 proteins -  
XX  
PS Claim 5; Page 104-108; 162pp; English.  
XX  
CC The invention relates to methods of altering the polypeptide levels in a  
CC cell, using proteins selected from S-phase kinase associated proteins 1  
CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the  
CC cullin/CDC53 family of proteins). The method is useful for altering the  
CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2  
CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for  
CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents  
CC that modulate interactions between SKP and target proteins are useful for  
CC treating tumours.  
XX  
SQ Sequence 239 AA;  
Query Match 14.5%; Score 159.5; DB 22; Length 239;  
Best Local Similarity 22.4%; Pred. No. 4.1e-09;  
Matches 47; Conservative 37; Mismatches 73; Indels 53; Gaps 7;  
QY 37 EYVHARLLRAGLSW-----SAPERASAPAG-----GRLEAVCY-- 69

```

Db      17 KYIHKYSQGYEMDAGDVGAAPGAPAPGIFSSQPGHTPHTAASRDVPARTSPLOTPTA 76
QY      70 -----VLLRLGDELBOIRSVYRNVARQIHI-PLQSEPVVTDAPFLA 109
Db      77 APCAAGAPALSPVPVPHVHLTLROAGDDFSRRYRDRFAEMSRQLHLNPFETAR---GREFAT 132
QY      110 VAGHIFSAGITGKVVSLYSAAAGLAVDCVROQAPAMVHALVDCIGEFVFKTLATWLR 169
Db      133 VVEELFRDGVNMGRIYAFEFEGVGCVESYNREMSPLVDIALMTEYLNHRHLHTWIODN 192
QY      170 GGMTDVLKCV-VSTKPGFRSHWL-VATLCS 197
Db      193 GGMDAFVELYGPSPMRPLDFESWLSKLTLS 222

```

## RESULT 11

```

AAB50537
ID      AAB50537 standard; Protein; 239 AA.
XX
AC      AAB50537;
XX
DT      16-MAR-2001 (first entry)
XX
DE      Human Bcl-2 protein sequence SEQ ID NO:2.
XX
KM      Human; Bcl-2; Bcl-XL; Bax; VDAC; apoptosis inhibitor; detection;
KW      apoptosis promoter; diagnosis.
XX
OS      Homo sapiens.
XX
PN      JP2000287689-A.
XX
PD      17-OCT-2000.
XX
PE      08-APR-1999; 99JP-0101888.
XX
PR      08-APR-1999; 99JP-0101888.
XX
PA      (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX
DR      WPI: 2001-065575/08.
XX
DR      N-PSDB; AAC90809.
XX
PT      Screening of an apoptosis inhibitor or promoter which can be used as a
PT      drug and a diagnostic agent for various diseases caused by apoptosis
PT      inhibition or apoptosis promotion -
XX
PS      Claim 11; Page 13-14; 22pp; Japanese.
XX
CC      The present invention describes a method for screening for an apoptosis
CC      inhibitor or an apoptosis promoter in which VDAC-1 liposome, an index
CC      substance which can pass VDAC and a sample are incubated and the change
CC      in the concentration of the index substance during the incubation is
CC      detected to judge the presence of apoptosis inhibitor or apoptosis
CC      promotion. The apoptosis inhibitor or the apoptosis promoter can be
CC      used as a drug and a diagnostic agent for various diseases caused by
CC      apoptosis inhibition or apoptosis promotion. The present sequence
CC      represents the human Bcl-2 protein, which is an apoptosis inhibitor
CC      used in the exemplification of the present invention.
XX
SQ      Sequence 239 AA;

```

```

Query Match      14.5%; Score 159.5; DB 22; Length 239;
Best Local Similarity 22.4%; Pred. No. 4.1e-09;
Matches 47; Conservative 37; Mismatches 73; Indels 53; Gaps 7;

```

```

QY      37 EYVHARLLRAGLSM-----SAPERASPAAG-----GRLAEVCT-- 69
Db      17 KYIHKYSQGYEMDAGDVGAAPGAPAPGIFSSQPGHTPHTAASRDVPARTSPLOTPTA 76
QY      70 -----VLLRLGDELBOIRSVYRNVARQIHI-PLQSEPVVTDAPFLA 109

```

```

Db      77 APCAAGAPALSPVPVPHVHLTLROAGDDFSRRYRDRFAEMSRQLHLNPFETAR---GREFAT 132
QY      110 VAGHIFSAGITGKVVSLYSAAAGLAVDCVROQAPAMVHALVDCIGEFVFKTLATWLR 169
Db      133 VVEELFRDGVNMGRIYAFEFEGVGCVESYNREMSPLVDIALMTEYLNHRHLHTWIODN 192
QY      170 GGMTDVLKCV-VSTKPGFRSHWL-VATLCS 197
Db      193 GGMDAFVELYGPSPMRPLDFESWLSKLTLS 222

```

## RESULT 12

```

AAW01020
ID      AAW01020 standard; Protein; 232 AA.
XX
AC      AAW01020;
XX
DT      18-DEC-1996 (first entry)
XX
DE      Apoptosis-blocking protein Bcl-2 mutant 80-6 (del80-86).
XX
KM      Apoptosis-regulating protein; Bcl-2; oncogene;
KW      adenovirus E1B 19K protein; cell death; cancer; tumour;
KW      immune disorder; diagnosis; therapy; B1p1; B1p3; B1p5; N1p1;
KW      N1p2; N1p3.
XX
OS      Synthetic.
XX
PN      EP733706-A2.
XX
PD      25-SEP-1996.
XX
PE      21-MAR-1996; 96EP-0104542.
XX
PR      21-MAR-1995; 95US-0408095.
XX
PA      (UYSL-) UNIV ST LOUIS.
XX
PI      Chinnadurai G;
XX
DR      WPI: 1996-427055/43.
XX
PT      Nucleic acids encoding apoptosis regulating proteins - useful for
PT      diagnosing and treating immune disorders, malignancies, etc.
XX
PS      Example 8; Page 34-35; 60pp; English.
XX
CC      The 80-6 mutant (AAW01020) of the bcl-2 oncogene product (AAW01018)
CC      lacks amino acids 80-86 of the native protein. This and other
CC      Bcl-2 mutants (see also AAW01019-21) were used in a two hybrid assay
CC      to examine the interactions between Bcl-2 and novel apoptosis-
CC      regulating proteins N1p1, N1p2 and N1p3 (AAW00997-99). 2 Motifs
CC      (AAW01003-04) on Bcl-2 were identified that are essential for
CC      interaction with the N1p proteins. These motifs show homology
CC      to motifs (AAW01005-06) identified on the adenovirus E1B 19K
CC      apoptosis-blocking protein (AAW01010).
XX
SQ      Sequence 232 AA;

```

```

Query Match      14.4%; Score 158; DB 17; Length 232;
Best Local Similarity 22.7%; Pred. No. 5.8e-09;
Matches 46; Conservative 37; Mismatches 74; Indels 46; Gaps 7;

```

```

QY      37 EYVHARLLRAGLSM-----SAPERASPAAG-----GRLAEVCT-- 69
Db      17 KYIHKYSQGYEMDAGDVGAAPGAPAPGIFSSQPGHTPHTAASRDVPARTSPLOTPTA 76
QY      70 -----VLLRLGDELBOIRSVYRNVARQIHI-PLQSEPVVTDAPFLAVAGHIFS 116
Db      77 APCAAGAPALSPVPVPHVHLTLROAGDDFSRRYRDRFAEMSRQLHLNPFETAR---GCFATVVEELFR 132
QY      117 AGITWCVVSLYSAAAGLAVDCVROQAPAMVHALVDCIGEFVFKTLATWLRRGGWTDVL 176

```

DB 133 DGVNMGRIVAFFFGVCMVESVNREMSPLVDNIALMTEYLNRHLHTWIONGMDAV 192  
QY 177 KCV-VSTKPGFRSHWL-VATLCS 197  
DB 193 ELYGFSMRPLDFPSWLSLTKLLS 215

## RESULT 13

AAW94347  
ID AAW94347 standard; Protein; 232 AA.

AAW94347;

DT 13-APR-1999 (first entry)

DE Human Bcl-2 mutant protein #80-6.

XX Human; Nip1; Nip2; Nip3; Bip1a; Bip5; Bip13; adenovirus; cell death;

XX viral infection; Bcl-2; protooncogene; mutational analysis; apoptosis;

XX E1B 19K protein; cell survival regulation.

OS Homo sapiens.

XX Synthetic.

PN US5858678-A.

PD 12-JAN-1999.

PF 21-MAR-1995; 95US-0408095.

PR 02-AUG-1994; 94US-0284139.

PR 21-MAR-1995; 95US-0408095.

PA (UTSL-) UNIV ST LOUIS.

PI Chinnadurai G;

DR WPI; 1999-152099/13.

XX Polypeptides that bind to anti-apoptotic proteins - useful for

PT protecting against cell death induced by viral infection and to

PT modulate response to physical and chemical stimuli

XX Example 8; Column 43-46; 41pp; English.

XX The present invention describes: (1) a method for regulating cell death,

CC comprising exposing an isolated cell to a polypeptide selected from

CC Nip1, Nip2, Nip3, Bip1a, Bip5 and Bip13; (2) a method for neutralising

CC the activity of the adenovirus E1B 19 kb protein, the Bcl-2 protein or

CC the BHRF-1 protein, comprising exposing an isolated cell to a

CC polypeptide as in (1); and (3) a method for detecting molecules that

CC bind to at least one polypeptide as in (1), comprising lysing cells,

CC exposing the lysate to the polypeptide and detecting any molecule-

CC polypeptide aggregates. The methods are useful for providing proteins

CC able to bind to other proteins known to regulate cell survival e.g. it

CC is known that E1B 19K protein provides a survival function similar to

CC the cellular protooncogene bcl-2 gene product which is able to block

CC apoptosis in haematopoietic B and T cells. The present sequence

CC represents a human Bcl-2 mutant protein from the present invention.

CC Sequence 232 AA;

QY Query Match 14.4%; Score 158; DB 20; Length 232;

DB Best Local Similarity 22.7%; Pred. No. 5.8e-09;

Matches 46; Conservative 37; Mismatches 74; Indels 46; Gaps 7;

QY 37 EYVHARLRAGISW-----SAPERASAPG-----GRLAVCT-- 69

DB 17 KYIHKLSORGYEMDAGVGAAPGAPGFFSSOPGHTPPAASRPVATSPLOQPA 76

QY 70 -----VLLRLDELEQIRPSVYRNAROLHT-PLQSEPVYDIAFLAVAGHIPS 116

DB 77 AFGSPVPVPHVHLTRQADDESRARRRDPFAEMSSQHLHLPFTAR-----GCFATVVEELFR 132

QY 117 AGITMGKVSLYSAAAGLAVDCVROAPAMVHALVDLCGEFVRKTLATWLRRGCTDVL 176  
DB 133 DGVNMGRIVAFFFGVCMVESVNREMSPLVDNIALMTEYLNRHLHTWIONGMDAV 192  
QY 177 KCV-VSTKPGFRSHWL-VATLCS 197  
DB 193 ELYGFSMRPLDFPSWLSLTKLLS 215

## RESULT 14

AAW87811  
ID AAW87811 standard; Protein; 236 AA.

AAW87811;

DT 10-MAR-1999 (first entry)

DE A murine Bcl-2 protein.

XX Human; Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;

XX bcl-2-related function; apoptosis; dimer; Bcl-XL; Mcl-1; Al.

OS Mus sp.

PN US5856171-A.

PD 05-JAN-1999.

PF 10-NOV-1994; 94US-0337646.

PR 10-NOV-1994; 94US-0337646.

PR 26-AUG-1993; 93US-0112208.

PR 25-MAY-1994; 94US-0248819.

PA (UNIW ) UNIV WASHINGTON.

PI Korsmeyer SJ;

DR WPI; 1999-105119/09.

XX DNA composition encoding bcl-2 two-hybrid and reporter system - for

PT identifying modulators of bcl-2 function

XX Example 10; Fig 7; 105pp; English.

XX The present sequence represents a murine Bcl-2 protein. The

CC specification also describes Bcl-2 associated proteins

CC designated Bax. The Bax protein is used in a composition which

CC comprises a bcl-2 family member polypeptide, a naturally occurring

CC Bax polypeptide and an antibody that binds to the Bax polypeptide.

CC The specification also describes a composition comprising a hybrid

CC protein and a bcl-2 family member having a BH1 domain and a BH2 domain;

CC another hybrid protein comprising a DNA-binding domain of the

CC transcriptional activator protein and a second bcl-2 family member

CC having a BH1 domain and a BH2 domain; and a reporter gene linked to a

CC transcriptional regulatory element whose transcriptional activity is

CC dependent on the presence or absence of a dimer of the two hybrid

CC proteins. The bcl-2 family members are selected from naturally occurring

CC Bcl-2, Bcl-XL, Bax, Mcl-1, Al, fragments thereof, and mutants having a

CC mutation in the BH1 and/or BH2 domain that alters intermolecular binding

CC of the two bcl-2 family members. The compositions are used to identify

CC modulators of bcl-2-related function, e.g. substances that inhibit

CC binding of Bax to bcl-2, which would be potentially useful as drugs

CC for modulating apoptosis.

QY Sequence 236 AA;

DB Query Match 14.3%; Score 157.5; DB 20; Length 236;

Matches 50; Conservative 37; Mismatches 79; Indels 57; Gaps 8;







GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:19:46 ; Search time 21.7493 seconds  
(without alignments)  
1610.532 Million cell updates/sec

Title: US-09-682-667-8  
Perfect score: 884  
Sequence: 1 MEVLRRSSVFYFAEIMDAFDR.....TLCSPGFRLKAFLLPER 170

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	860	97.3	170	11 088857	088857 rattus norv
2	852.5	96.4	213	4 Q9UJ32	Q9UJ32 rattus norv
3	828.5	93.7	213	11 035425	035425 rattus norv
4	783	88.6	212	4 Q9UWX3	Q9UWX3 homo sapien
5	681.5	77.1	213	13 091812	Q91812 gallus gall
6	675.5	76.4	213	13 09DGJ5	Q9DGJ5 gallus gall
7	178	20.1	299	5 Q8TRX5	Q8TRX5 drosophila
8	178	20.1	313	5 Q9NGX3	Q9NGX3 drosophila
9	169.5	19.2	247	5 Q9V612	Q9V612 drosophila
10	169	19.1	300	5 Q9V9C8	Q9V9C8 drosophila
11	138	15.6	317	5 Q95083	Q95083 drosophila
12	129.5	14.6	236	11 Q923R6	Q923R6 cricetus
13	108.5	12.3	192	13 Q919N4	Q919N4 brachydanio
14	108.5	12.3	219	11 Q99N36	Q99N36 mus musculu
15	108.5	12.3	235	11 Q35843	Q35843 mus musculu
16	107.5	12.2	233	11 Q35844	Q35844 mus musculu

17	106.5	12.0	238	13 Q90298	Q90298 brachydanio
18	104.5	11.8	233	6 Q8SQ42	Q8SQ42 felis silve
19	104	11.8	188	11 Q9QWX2	Q9QWX2 mus musculu
20	104	11.8	217	11 Q99N35	Q99N35 mus musculu
21	103	11.7	180	6 Q9BDD5	Q9BDD5 bos taurus
22	103	11.7	233	6 Q9MZS7	Q9MZS7 ovis aries
23	103	11.7	233	6 Q9N1A2	Q9N1A2 sus scrofa
24	102	11.5	188	4 Q9H1R6	Q9H1R6 homo sapien
25	102	11.5	233	6 Q9MYW4	Q9MYW4 oryctolagus
26	101	11.4	180	6 Q9BDX7	Q9BDX7 bos taurus
27	99	11.2	193	11 Q86996	Q86996 rattus norv
28	99	11.2	221	13 Q98U13	Q98U13 xenopus lae
29	98.5	11.1	163	6 Q9MZS6	Q9MZS6 ovis aries
30	98	11.1	204	13 Q9QZH2	Q9QZH2 xenopus lae
31	97	11.0	178	11 Q9CYW5	Q9CYW5 mus musculu
32	97	11.0	179	4 Q9NKG7	Q9NKG7 homo sapien
33	94	10.6	173	11 Q9UKL3	Q9UKL3 rattus norv
34	93	10.5	172	11 Q95177	Q95177 mus musculu
35	92	10.4	114	4 Q9NR76	Q9NR76 homo sapien
36	92	10.4	149	6 Q9CMG7	Q9CMG7 ovis aries
37	92	10.4	173	4 Q8WZ49	Q8WZ49 homo sapien
38	92	10.4	192	6 Q8S043	Q8S043 felis silve
39	90	10.2	209	11 Q9UK59	Q9UK59 rattus norv
40	89.5	10.1	172	11 Q95179	Q95179 mus musculu
41	86	9.7	2497	16 Q8XYB9	Q8XYB9 raietonia s
42	85	9.6	175	11 Q925A9	Q925A9 rattus norv
43	85	9.6	177	2 Q9AEZ3	Q9AEZ3 frankia sp
44	85	9.6	185	12 Q8YBG1	Q8YBG1 hepatitis b
45	84.5	9.6	182	16 Q8XUQ3	Q8XUQ3 raietonia s

## ALIGNMENTS

RESULT 1  
ID 088857 PRELIMINARY; PRT; 170 AA.  
AC 088857;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Bcl-2-related ovarian killer protein.  
GN BOK.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=OVARY;  
RX MEDLINE=98024143; PubMed=9356461;  
RA Hsu S.Y., Kaipia A., McGee E., Lomeli M., Hsueh A.J.W.;  
RT "BOK is a pro-apoptotic bcl-2 protein with restricted expression in  
reproductive tissues and heterodimerizes with selective anti-apoptotic  
bcl-2 family members.";  
RT Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=OVARY;  
RA Hsu S.Y., Hsueh A.J.W.;  
RT "A splicing variant of the Bcl-2 member BOK with a truncated BH3  
domain induces apoptosis without dimerization with anti-apoptotic Bcl-  
2 proteins.";  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF051093; AAC61928.1; -;  
DR InterPro: IPR000712; Bcl2.BH.  
DR InterPro: IPR002475; BCL2\_family.  
DR Pfam: PF00452; Bcl-2; 1.  
DR SMART: SM00337; BCL; 1.  
DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
SQ SEQUENCE 170 AA; 18729 MW; 15E54361F448CF16 CRC64;  
Query Match 97.3% Score 860; DB 11; Length 170;

```

Best Local Similarity 96.2%; Pred. No. 4,5e-72;
Matches 167; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEVLRSSVFAAEIMDAFDRWPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASAP 60
   |||||||
Db 1 MEVLRSSVFAAEIMDAFDRSPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASAP 60

QY 61 GGRLAEVCTVLLRLGITMGKVVSLYSAAGLAVDCVROAOPAMVHALVDCGGEFVKTLLA 120
   |||||||
Db 61 GGRLAEVCTVLLRLGITMGKVVSLYSAAGLAVDCVROAOPAMVHALVDCGGEFVKTLLA 120

QY 121 TWLRRGGMTDVLKCVSTKPGFRSHMLVATLCSFGRLKAAFFLLPER 170
   |||||||
Db 121 TWLRRGGMTDVLKCVSTKPGFRSHMLVATLCSFGRLKAAFFLLPER 170

RESULT 2
Q9UL32 PRELIMINARY: PRT: 213 AA.
AC Q9UL32;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Bcl-2 related ovarian killer.
GN BOK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hsu S.Y., Hsueh A.J.W.;
RT "CDNA cloning of the human Bcl gene."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF089746; AAF09129.1;
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
SQ SEQUENCE 213 AA; 23540 MW; 59509F8C730517F CRC64;

Query Match 96.4%; Score 852.5; DB 4; Length 213;
Best Local Similarity 79.8%; Pred. No. 2.9e-71;
Matches 170; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

QY 1 MEVLRSSVFAAEIMDAFDRWPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASAP 60
   |||||||
Db 1 MEVLRSSVFAAEIMDAFDRWPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASAP 60

QY 61 GGRLAEVCTVLLRL-----GTT 77
   |||||||
Db 61 GGRLAEVCTVLLRLGDELEQIRPSVYRNVARQLHPILOSEPVVTDATLAVAGHIFSAGIT 120

QY 78 WGVVSLYSAAGLAVDCVROAOPAMVHALVDCGGEFVKTLLATWLRGGMTDVLKCV 137
   |||||||
Db 121 WGVVSLYSAAGLAVDCVROAOPAMVHALVDCGGEFVKTLLATWLRGGMTDVLKCV 180

QY 138 STKPGFRSHMLVATLCSFGRLKAAFFLLPER 170
   |||||||
Db 181 STKPGFRSHMLVATLCSFGRLKAAFFLLPER 213

RESULT 3
Q35425 PRELIMINARY: PRT: 213 AA.
AC Q35425;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Bcl-2-related ovarian killer protein.
GN BOK OR BOKL OR BOK OR MTD.
OS Rattus norvegicus (Rat), and

```

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116, 10090;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; STRAIN=SPRAGUE-DAWLEY; TISSUE=OVARY, TESTIS, AND UTERUS;
RX MEDLINE=98024143; PubMed=9356461;
RA Hsu S.Y., Kaipia A., McGee E., Iomeli M., Hsueh A.J.W.;
RT "Bcl-2 is a pro-apoptotic Bcl-2 protein with restricted expression in
reproductive tissues and heterodimerizes with selective anti-apoptotic
Bcl-2 family members."
RT Proc. Natl. Acad. Sci. U.S.A. 94:12401-12406(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; STRAIN=SPRAGUE-DAWLEY; TISSUE=OVARY, TESTIS, AND UTERUS;
RA Hsu S.Y., Hsueh A.J.W.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse;
RA Inohara N., Ekheraee D., Garcia I., Carrio R., Merino J., Merry A.,
Chen S., Nunez G.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF027707; AAC53582.1;
DR MGD; MGI:1858494; BOK.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR002475; Bcl2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
SQ SEQUENCE 213 AA; 23456 MW; F8755C45CB05D626 CRC64;

Query Match 93.7%; Score 828.5; DB 11; Length 213;
Best Local Similarity 78.4%; Pred. No. 4.8e-69;
Matches 167; Conservative 0; Mismatches 3; Indels 43; Gaps 1;

QY 1 MEVLRSSVFAAEIMDAFDRWPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASAP 60
   |||||||
Db 1 MEVLRSSVFAAEIMDAFDRSPTDKELVAQAKALGREYVHARLLRAGLSWSAPERASAP 60

QY 61 GGRLAEVCTVLLRL-----GTT 77
   |||||||
Db 61 GGRLAEVCTVLLRLGDELEQIRPSVYRNVARQLHPILOSEPVVTDATLAVAGHIFSAGIT 120

QY 78 WGVVSLYSAAGLAVDCVROAOPAMVHALVDCGGEFVKTLLATWLRGGMTDVLKCV 137
   |||||||
Db 121 WGVVSLYSAAGLAVDCVROAOPAMVHALVDCGGEFVKTLLATWLRGGMTDVLKCV 180

QY 138 STKPGFRSHMLVATLCSFGRLKAAFFLLPER 170
   |||||||
Db 181 STKPGFRSHMLVATLCSFGRLKAAFFLLPER 213

RESULT 4
Q9UMX3 PRELIMINARY: PRT: 212 AA.
AC Q9UMX3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Bcl-2-related ovarian killer protein (Similar to Bcl-2-related ovarian
killer protein-like-PENDING) (BCL-2-related ovarian killer
protein-like).
GN BOK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang H.;

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RESULT	5			
ID	091812	PRELIMINARY:	PRT:	213 AA.
AC	091812;			
DT	01-OCT-2000 (TREMBlrel. 15, Created)			
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)			
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)			
DE	Bcl-2-related ovarian killer protein.			
OS	Gallus gallus (chicken).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Archosauromia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20487164; PubMed=11034351;			
RA	Zhang H., Holzgrefe W., De Geylet C.;			
RT	"Evolutionarily conserved Bcl proteins in the Bcl-2 family. "			
RL	FEBS Lett. 480:311-313(2000) .			
DR	EMBL: AF275944; AAF81282.1; -			
DR	InterPro: IPR000712; Bcl2.BH.			
DR	InterPro: IPR002475; BCL2_family.			
DR	Pfam: PF00452; Bcl-2; 1.			
DR	SMART: SM00357; BCL_1.			
DR	PROSITE: PS50062; BCL2_FAMILY; 1.			
QO	SEQUENCE 213 AA; 23619 MW; B3AF7049F25442B3 CRC64;			

Query Match	77.1%;	Score 681.5;	DB 13;	Length 213;
Best Local Similarity	61.5%;	Pred. No. 2e-55;		

	Query Match	76.4%	Score 675.5;	DB 13;	Length 213;
	Best Local Similarity	60.6%;	Pred. No. 7e-55;		
	Matches 129;	Conservative 19;	Mismatches 22;	Indels 43;	Gaps 1.
QY	1 MEVLRRSSVFAAEITDADFRMPTDKDELVAQAALGREVYHARLLRAGLSMSAPERASPA	60			
	:                     :				
Db	1 MEVLRRSSVFAAEVEFBRSPTDKELVSQAALCRDYINSLIRXGVSMSPENHTPP	60			
QY	61 GGRLAENVCTVLLRL-----	-GIT 77			
Db	61 GGKLAENVSAITLRLDELEIYIPPNRYRNRIARLNISLHSEITYVTDTAFLLAQAQIFLAGIT	120			
QY	78 WGVVSTLSAAGLAAGLVDCVRQAOPAMVHALVDCLGEFYFKTLATWLRRGSGTDLKCV	137			
Db	121 WGVVSLTAAGAAGLVAVDCVRNHAQPAMVHTIYDCLGEFAYKTLVTWMLKRGGNADITKC	180			
QY	138 STKGFSRHMLVATLCFSGRFLLKAQFTLLP	170			
Db	181 STDPSLRSHMLEVAACVSFGHFLLAKFFEVLLP	213			
RESULT 7					
Q8r8y5	ID	Q8r8y5	PRELIMINARY;	PRT;	299 AA.
AC	Q8r8y5				
DT	01-JUN-2002	(TREMBLrel. 21,	Created)		
OT	01-JUN-2002	(TREMBLrel. 21,	Last sequence update)		
T	01-JUN-2002	(TREMBLrel. 21,	Last annotation update)		

DE ARI6536P.  
 GN BUFRY.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Stapleton M., Brokstein P., Hong L., Abbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nuno J., Pacleb J., Patagas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celinker S.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY075219; AAL68086.1; -  
 SO SEQUENCE 299 AA; 33379 MW; 7FB125A6B7323B23 CRC64;

Query Match 20.1%; Score 178; DB 5; Length 299;  
 Best Local Similarity 26.9%; Pred. No. 1.2e-08;  
 Matches 56; Conservative 24; Mismatches 62; Indels 66; Gaps 8;

OY 25 KEVVAQAKALGVEYHARLRAGL-----SNAP----- 53  
 DB 87 QDIIISQGRCLGCHYIKRRLRNRSGLEFNKKLGLQIRISLIGSTSMGIVRDVFPVAVYLGDEL 146  
 OY 54 ERASPA-----PGGR-----LAECVTLLRLGITMGKVVSLYSAAAGL 91  
 DB 147 ERMHRIINGVARQICRNPGGEGFHPDPAVSLLLGAVNGRELFPVELTWSKVISLFLAAGL 206  
 OY 92 AVDCVRQAQAPAMVAHVDCLGFEVRKTLATWLRRRGW---TDVLCVCVSTKPGFRSHW 147  
 DB 207 SVDCVRQCHPEYLPKLMESVSEVIEDLVPMINENGWSGINTHVLPTTNSLNP---LEW 263  
 OY 148 LVATL-CSEG-----RLKAAFFELLPE 169  
 DB 264 TTLVIGVFGLLVFMILRFTFNLIVPK 291

RESULT 8  
 O9NGX3 PRELIMINARY; PRT; 313 AA.  
 AC O9NGX3;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Bcl-2-like protein BUFRY (Fragment).  
 GN BUFRY OR CG8238.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=2013510; PubMed=10684252;  
 RA Colussi P.A., Quinn L.M., Huang D.C., Coombe M., Read S.H.,  
 RA Richardson H., Kumar S.;  
 RL "Debel, a proapoptotic bcl-2 homologue, is a component of the  
 RT Drosophila melanogaster cell death machinery."  
 RL J. Cell Biol. 148:703-714(2000).  
 DR EMBL: AF237864; AAF44120.1; -;  
 DR HSPB; Q07817; IMAZ.  
 DR Flybase: FBgn0040491; BUFRY.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PSS0062; BCL2\_FAMILY; 1.  
 DR NON TER 1  
 SO SEQUENCE 313 AA; 34909 MW; 775A1FDD5B678F CRC64;

Query Match 20.1%; Score 178; DB 5; Length 313;  
 Best Local Similarity 26.9%; Pred. No. 1.2e-08;  
 Matches 56; Conservative 24; Mismatches 62; Indels 66; Gaps 8;  
 OY 25 KEVVAQAKALGVEYHARLRAGL-----SNAP----- 53  
 DB 101 QDIIISQGRCLGCHYIKRRLRNRSGLEFNKKLGLQIRISLIGSTSMGIVRDVFPVAVYLGDEL 160  
 OY 54 ERASPA-----PGGR-----LAECVTLLRLGITMGKVVSLYSAAAGL 91  
 DB 161 ERMHRIINGVARQICRNPGGEGFHPDPAVSLLLGAVNGRELFPVELTWSKVISLFLAAGL 220  
 OY 92 AVDCVRQAQAPAMVAHVDCLGFEVRKTLATWLRRRGW---TDVLCVCVSTKPGFRSHW 147  
 DB 221 SVDCVRQCHPEYLPKLMESVSEVIEDLVPMINENGWSGINTHVLPTTNSLNP---LEW 277  
 OY 148 LVATL-CSEG-----RLKAAFFELLPE 169  
 DB 278 TTLVIGVFGLLVFMILRFTFNLIVPK 305

RESULT 9  
 O9V612 PRELIMINARY; PRT; 247 AA.  
 AC O9V612;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE CG8238 protein.  
 GN BUFRY OR CG8238.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Abbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalaia M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Jai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon R., Nuskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,



DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS50157; ZINC\_FINGER\_C2H2\_2; 4.  
 KW DNA-binding; zinc-finger.  
 FT CONFLICT 1 86 MISSING (IN REF. 4).  
 FT CONFLICT 215 215 I -> V (IN REF. 1).  
 FT CONFLICT 217 217 C -> R (IN REF. 4).  
 SQ SEQUENCE 300 AA; 32940 MM; FE29E0ADC3D0942 CRC64;

Query Match 19.1%; Score 169; DB 5; Length 300;  
 Best Local Similarity 27.6%; Pred. No. 8e-08;  
 Matches 43; Conservative 17; Mismatches 44; Indels 52; Gaps 3;

QY 26 ELVAQAALGEEYHARLRAG-LSWSAPER----- 55  
 DB DIINGKCLCGQYIRARLRAGVLRNRYORLRNLDPGSSHYVEVPALNSMGEELR 155  
 QY 56 -----ASAPGGRLAE-----VCTVLRIGITWGKVVSLXSAAGLAV 93  
 DB 156 MHPVYTNISRLSRAPGELSDMAPMLNLVAKDLFRSSITWGKITSIFAVCGGFAI 215  
 QY 94 DCVROAQPAMVHALVDCGEEFVRK-TLATWLRRRG 129  
 DB 216 DCVROGHFDYLOCLIDGLAEITIEDLVYWLIDNGW 251

## RESULT 11

095083 PRELIMINARY; PRT; 317 AA.  
 ID 095083  
 AC 095083  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE GH01265P.  
 DE DEBCL OR CG12397.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY.  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda C.J.,  
 RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celisner S.;  
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AY058249; AAL13478.1; -  
 DR FlyBase: FBgn0029131; debcl.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 SQ SEQUENCE 317 AA; 34649 MM; 46B22FED1CC6F01F CRC64;

Query Match 15.6%; Score 138; DB 5; Length 317;  
 Best Local Similarity 26.8%; Pred. No. 6.3e-05;  
 Matches 42; Conservative 18; Mismatches 43; Indels 54; Gaps 4;

QY 26 ELVAQAALGEEYHARLRAG-LSWSAPER----- 55  
 DB DIINGKCLCGQYIRARLRAGVLRNRYORLRNLDPGSSHYVEVPALNSMGEELR 155  
 QY 56 -----ASAPGGRLAE-----VCTVLRIGITWGKVVSLXSAAGLAV 93  
 DB 156 MHPVYTNISRLSRAPGELSDMAPMLNLVAKDLFRSSITWGKITSIFAVCGGFAI 215  
 QY 94 DCVROAQPAMVHALVDCGEEFVRK-TLATWLRRRG 129  
 DB 216 DCVROGHFDYLOCLIDGLAEITIEDLVYWLIDNGW 252

## RESULT 12

0923R6 PRELIMINARY; PRT; 236 AA.  
 ID 0923R6  
 AC 0923R6  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE B-cell lymphoma protein 2.  
 GN BCL2.  
 OS Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetulus.  
 NC NCBI\_TaxID=10030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lai D.Z., Chen W., Wang H.T.;  
 RT "Construction of a robust CHO cell line for biopharmaceutical use."  
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF404339; AAK92201.1; -  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR InterPro: IPR002475; Bcl2\_family.  
 DR InterPro: IPR004723; Bcl2\_freg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR TIGRFAMS: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; UNKNOWN\_1.  
 DR PROSITE: PS01258; BH2; UNKNOWN\_1.  
 DR PROSITE: PS01259; BH3; UNKNOWN\_1.  
 DR PROSITE: PS01260; BH4\_1; UNKNOWN\_1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 SQ SEQUENCE 236 AA; 26500 MM; BEDF052EF32CA8B8 CRC64;

Query Match 14.6%; Score 129.5; DB 11; Length 236;  
 Best Local Similarity 18.9%; Pred. No. 0.00026;  
 Matches 40; Conservative 26; Mismatches 55; Indels 91; Gaps 4;

QY 28 VAQAKALG-----REYVHARLRAGLSW-----SAPERASPARG----- 61  
 DB 1 MAQAGRTGYDNRREIVMKIYHKLSGRYEMDVGDVDAFLGAAPYGFISFPESPPTPA 60  
 QY 62 ----- 61  
 DB 61 VHRDWAARTSPLRPVATTTGPTLSPVPVHLTLRRAGDDESRRYRDFAEWSSQLHLP 120  
 QY 62 -----GLAEVCTVLRIGITWGKVVSLXSAAGLAVDCVROAQPAMVHALVDCGEEFVRK 117  
 DB 121 FTARGREFATVVEELFRDGVNMGRIVAFFEGVCVNCESVNRNEMSPVDVNIAMTETYNR 180  
 QY 118 TLATWLRRRGMTDLKCV-VSTKPGFRSHWL 148  
 DB 181 HLHTWIDQNGMDAFLVELYGPVRLPFDPSWL 212

## RESULT 13

0919N4 PRELIMINARY; PRT; 192 AA.  
 ID 0919N4  
 AC 0919N4  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Bax.  
 GN BAX.  
 OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NC NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE-20373792; PubMed-10917738;  
 RA Inohara N., Nunez G.;  
 RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish."  
 RU Cell Death Differ. 7:509-510(2000).  
 DR EMBL; AF231015; AAF66960.1; -.  
 DR HSSP; P53563; IAF3.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR002475; BCL2\_family.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 SQ SEQUENCE 192 AA; 21401 MW; 8A71A630A56FDC32 CRC64;

Query Match 12.3%; Score 108.5; DB 13; Length 192;  
 Best Local Similarity 21.0%; Pred. No. 0.019; Mismatches 64; Indels 35; Gaps 4;  
 Matches 34; Conservative 29;

QY 6 RSSVFAEIMDAFDRWPTDELVAQAKALGREYVHARLLRAGLSWSPAPGRLA 65  
 DB 45 RSLGGVELCD-----PSHKRLAQCLQIGDELGNAGQSMLN-----NSNQ 88  
 QY 66 EYCTVLLRIG-----ITGKVSLYSAAAGLAVDCVROQAPAMVHALVDCIGEFVK 117  
 DB 89 PQQDFVIRVAREIFSDGKFNMGVVALFYFACRLVTKAISTRVPDIIRIISWTMSYIOE 148  
 QY 118 TLATLRRRGWTDVLCVSTKPGFRSHWLVAATLCSFGRL 159  
 DB 149 HYINMIREQGM-----DGIIRSFGTPTMOTVGFEL 179

RESULT 14  
 Q99N36 PRELIMINARY; PRT; 219 AA.  
 AC Q99N36;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE B-cell leukemia/Lymphoma x-gamma (Fragment).  
 GN BCLX.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVT;  
 RA Yang X.-F., Cantor H.;  
 RT "Novel cDNA structure and genomic organization of apoptosis regulatory gene Bcl-x-gamma."  
 RT Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF133279; AAK15454.1; -.  
 DR EMBL; AF133281; AAK15454.1; JOINED.  
 DR HSSP; P53563; IAF3.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR002475; BCL2\_family.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 219 AA; 24224 MW; EB352EC4CPA6AF5 CRC64;

Query Match 12.3%; Score 108.5; DB 11; Length 219;  
 Best Local Similarity 23.0%; Pred. No. 0.022; Mismatches 43; Indels 15; Gaps 3;  
 Matches 25; Conservative 17;

QY 66 EYCTVLLRIGITWGVSLYSAAAGLAVDCVROQAPAMVHALVDCIGEFVKRLATWLR 125  
 DB 109 QVYNELFRQGVNMGRIVAFPSFGALCVESVDKEMQVLVSRIASMTATLNDHLEPWIOE 168  
 QY 126 RSGM-----TDVLKCVVSTKPGFRSH-----WLVAAT 151

DB 169 NGMGVSGGTPLRVFRRLVQV-PGVAEHVCDPSLWEVET 207

RESULT 15  
 O35843 PRELIMINARY; PRT; 235 AA.  
 AC O35843;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Bcl-x-gamma.  
 GN BCL2L.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B6/CBA; TISSUE=THYMUS;  
 RX MEDLINE=98051053; PubMed=9390687;  
 RA Yang X.-F., Weber G.F., Cantor H.;  
 RT "A novel Bcl-x isoform connected to the T cell receptor regulates apoptosis in T cells."  
 RT Immunity 7:629-639(1997).  
 RL EMBL; U51277; AAC53458.1; -.  
 DR HSSP; P53563; IAF3.  
 DR MGD; MGI:88139; Bcl2L.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH.  
 DR InterPro; IPR002475; BCL2\_family.  
 DR InterPro; IPR004725; Bcl2\_reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR TIGRPFAMs; TIGR00865; bcl-2; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 SQ SEQUENCE 235 AA; 26122 MW; 649D914C2D5378F6 CRC64;

Query Match 12.3%; Score 108.5; DB 11; Length 235;  
 Best Local Similarity 25.0%; Pred. No. 0.024; Mismatches 43; Indels 15; Gaps 3;  
 Matches 25; Conservative 17;

QY 66 EYCTVLLRIGITWGVSLYSAAAGLAVDCVROQAPAMVHALVDCIGEFVKRLATWLR 125  
 DB 125 QVYNELFRQGVNMGRIVAFPSFGALCVESVDKEMQVLVSRIASMTATLNDHLEPWIOE 184  
 QY 126 RSGM-----TDVLKCVVSTKPGFRSH-----WLVAAT 151  
 DB 185 NGMGVSGGTPLRVFRRLVQV-PGVAEHVCDPSLWEVET 223

Search completed: April 29, 2003, 11:25:41  
 Job time : 22.7493 secs





GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: April 29, 2003, 11:18:26 ; Search time 5.99217 Seconds  
(without alignments)  
1176.699 Million cell updates/sec

Title: US-09-682-667-8  
Perfect score: 884  
Sequence: 1 MEVLRRSSVFAEIMDAFDR.....TLCSEGRFLKAFLLPER 170

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : SwissProt.40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	140	15.8	236 1	BCL2_RAT
2	133	15.0	239 1	BCL2_HUMAN
3	132	14.9	229 1	BCL2_BOVIN
4	131	14.8	236 1	BCL2_CRIO
5	130	14.7	236 1	BCL2_MOUSE
6	115.5	13.1	233 1	BCL2_CHICK
7	112.5	12.7	228 1	ARL_XENLA
8	104.5	11.8	229 1	BCLX_CHICK
9	104	11.8	233 1	BCLX_MOUSE
10	104	11.8	233 1	BCLX_RAT
11	103	11.7	233 1	BCLX_PIG
12	102	11.5	233 1	BCLX_HUMAN
13	100	11.3	218 1	BAXB_HUMAN
14	99	11.2	193 1	BCLW_MOUSE
15	98	11.1	204 1	ARL1_XENLA
16	95	10.7	192 1	BAXA_HUMAN
17	95	10.7	193 1	BCLW_HUMAN
18	95	10.7	211 1	BAK_HUMAN
19	94	10.6	192 1	BAXA_MOUSE
20	94	10.6	192 1	BAXA_RAT
21	92.5	10.5	143 1	BAKD_HUMAN
22	92	10.4	192 1	BAXA_BOVIN
23	90	10.2	208 1	BAK_MOUSE
24	85.5	9.7	172 1	BEL1_MOUSE
25	85	9.6	211 1	BAK2_HUMAN
26	84	9.5	535 1	SSDH_HUMAN
27	83	9.4	1115 1	CARB_MYCTU
28	81	9.2	416 1	CHRA_PSEAE
29	77.5	8.8	2291 1	SPCB_PSEAE
30	77	8.7	175 1	BFL1_HUMAN
31	76.5	8.7	2128 1	SPCB_MOUSE
32	76	8.6	185 1	CORA_HPBVT
33	76	8.6	212 1	CORA_HPBVT

34	76	8.6	370 1	ID12_PYPAB	Q9uzs9 pyrococcus
35	76	8.6	1300 1	IRR_MOUSE	O9wt14 mus musculu
36	75.5	8.5	1121 1	CARB_MYCLE	O9ccr2 mycobacteri
37	75.5	8.5	2564 1	SPCO_HUMAN	O9t254 homo sapien
38	75	8.5	401 1	PLIC_PSEPU	P36641 pseudomonas
39	74.5	8.4	516 1	YAKT_RHISN	P55538 rhizobium s
40	74	8.4	185 1	CORA_HPBVT	P03148 hepatitis b
41	74	8.4	297 1	NADC_HUMAN	O15274 homo sapien
42	74	8.4	2137 1	YMH2_HUMAN	P11277 homo sapien
43	73.5	8.3	378 1	YMH2_MYCTU	O10400 mycobacteri
44	73.5	8.3	539 1	TCP2_CAEBL	P46550 caenorhabdi
45	73.5	8.3	610 1	RHO_MYCLE	P45835 mycobacteri

## ALIGNMENTS

RESULT 1  
ID BCL2\_RAT  
AC P49950; 062837; 064032;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptosis regulator Bcl-2.  
GN BCL2 OR BCL-2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=94193015; PubMed=8144041;  
RA Sato T., Irie S., Krajewski S., Reed J.C.;  
RT "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";  
RL Gene 140:291-292(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Ovary;  
RX MEDLINE=95129487; PubMed=7828536;  
RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;  
RT "Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xl-long messenger ribonucleic acid levels.";  
RL Endocrinology 136:232-241(1995).  
RN [3]  
RP SEQUENCE OF 19-172 FROM N.A.  
RX MEDLINE=95059917; PubMed=7969891;  
RA Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H., Lindholm D.;  
RT "bcl-2 messenger RNA is localized in neurons of the developing and adult rat brain.";  
RL Neuroscience 61:165-177(1994).  
CC -i- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1).  
CC -i- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-xL. Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (by similarity). Also interacts with APAF-1 and RAF-1 (by similarity).  
CC -i- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.  
CC -i- TISSUE SPECIFICITY: Expressed in a variety of tissues, with highest levels in reproductive tissues. In the adult brain, expression is localized in mitral cells of the olfactory bulb, granule and pyramidal neurons of hippocampus, pontine nuclei, cerebellar granule neurons, and in ependymal cells. In prenatal

```
CC brain, expression is higher and localized in the neuroepithelium
CC and in the cortical plate.
CC -1- DOMAIN: The Bcl-2 domain is required for anti-apoptotic activity and
CC for interaction with RAF-1 (By similarity).
CC -1- PPM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl-2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle. In the absence of
CC growth factors, Bcl-2 appears to be phosphorylated by other protein
CC kinases such as ERKs and stress-activated kinases.
CC Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
CC -1- PPM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the Bcl-2 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity (By similarity).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: U14680; AAA53662.1; -
DR EMBL: U14964; AAA77687.1; -
DR EMBL: S74122; - NOT_ANNOTATED_CDS.
DR HSSP: Q07817; IMAZ.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR TIGRFAMs: TIGR00865; bcl-2; 1.
DR PROSITE: PSS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01256; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PSS0063; BH4_2; 1.
DR Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
KW DOMAIN
FT DOMAIN 10 30 BH4.
FT DOMAIN 90 104 BH3.
FT DOMAIN 133 152 BH1.
FT DOMAIN 184 199 BH2.
FT TRANSMEM 209 230
FT SITE 34 35 POTENTIAL.
FT MOD_RES 70 70 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT CONFLICT 42 42 A -> R (IN REF. 2).
FT CONFLICT 157 157 E -> G (IN REF. 1).
FT CONFLICT 164 164 S -> Y (IN REF. 2).
FT CONFLICT 212 212 L -> O (IN REF. 2).
SQ SEQUENCE 236 AA; 26622 MW; E7686CB9071A872A CRC64;
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Query Match 15.8%; Score 140; DB 1; Length 236;
Best Local Similarity 20.5%; Pred. No. 1.5e-06;
Matches 45; Conservative 26; Mismatches 56; Indels 92; Gaps 5;
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OY 28 VAQKALG-----REYVARLLRAGISW-----SAPEASAPAC----- 61
DB 1 MAQAGRGYDNRREIVMYKHYKLSQRYGEMDTGDEDSAPLRAAPPGIFQPSNRTPA 60
OY 62 ----- 61
DB 61 VHRDTARTSLRPLVANAGPALSPVPVYHLTLRRAGDPSRRYRRDFAMMSQLHLTP 120
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OY 62 -----GRLAECTVLLRLGITWGVSYSAAGLAVDCAQAPAMHATVDCIGFEVRK 117
DB 121 FTAGRAFATVVEELFRQVMNGRIVAFFEGVCVSEVNMSPVDNIAIMMTETLNR 180
OY 118 TLATWLRRRGGTVDYLCV-VSTPGRSHWL-VATLCS 154
DB 181 HLHTWIDONGMDAFVELYGPSMRPLDFSWLSIKTLIS 219

RESULT 2
BCL2_HUMAN
ID BCL2_HUMAN STANDARD; PRT; 239 AA.
AC P10415; P10416; Q16197; Q13842;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RX MEDLINE=86259760; PubMed=3523487;
RA Tsujimoto Y., Croce C.M.;
RT "Analysis of the structure, transcripts, and protein products of
RT bcl-2, the gene involved in human follicular lymphoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
RN [2]
RP REVISTIONS TO 96; 110 AND 237.
RX MEDLINE=92375724; PubMed=1508712;
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression
RT in a variety of tissues including lymphoid and neuronal organs in
RT adult and embryo.";
RL Nucleic Acids Res. 20:4187-4192(1992).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=87002488; PubMed=2875799;
RA Cleary M.L., Smith S.D., Sklar J.;
RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-
RT 2/immunoglobulin transcript resulting from the t(14;18)
RT translocation.";
RL Cell 47:19-28(1986).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=88196071; PubMed=2834197;
RA Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.,
RA Goldman P., Korsmeyer S.J.;
RT "Alternative promoters and exons, somatic mutation and deregulation
RT of the Bcl-2-Ig fusion gene in lymphoma.";
RL EMBO J. 7:123-131(1988).
RN [5]
RP SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS NHL.
RX MEDLINE=92096610; PubMed=1339299;
RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.;
RT "Frequent incidence of somatic mutations in translocated BCL2
RT oncogenes of non-Hodgkin's lymphomas.";
RL Blood 79:229-237(1992).
RN [6]
RP SUBCELLULAR LOCATION.
RX MEDLINE=91066924; PubMed=2250705;
RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.;
RT "Bcl-2 is an inner mitochondrial membrane protein that blocks
RT programmed cell death.";
RL Nature 348:334-336(1990).
RN [7]
RP MUTAGENESIS.
RX MEDLINE=94239528; PubMed=8183370;
RA Yin X.-M., Oltvai Z.N., Korsmeyer S.J.;
RT "BH1 and BH2 domains of Bcl-2 are required for inhibition of
```

RT apoptosis and heterodimerization with Bax.";  
 RL Nature 369:321-323(1994).  
 RN [8]  
 RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.  
 RX MEDLINE=98057466; PubMed=9395403;  
 RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,  
 Rao K., Hardwick J.M.;  
 RT "Conversion of Bcl-2 to a Bax-like death effector by caspases.";  
 RL Science 278:1966-1968(1997).  
 RN [9]  
 RP REVIEW ON PHOSPHORYLATION.  
 RX MEDLINE=21260650; PubMed=11368354;  
 RA Ruvoilo P.P., Deng X., May W.S.;  
 RT "Phosphorylation of Bcl2 and regulation of apoptosis.";  
 RL Leukemia 15:515-522(2001).  
 RN [10]  
 RP PHOSPHORYLATION BY ASK1/JNK1.  
 RX MEDLINE=20036804; PubMed=10567572;  
 RA Yamamoto K., Ichijo H., Korsmeyer S.J.;  
 RT "Bcl-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal  
 RT protein kinase pathway normally activated at G(2)/M.";  
 RL Mol. Cell. Biol. 19:8469-8478(1999).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (Apaf-1).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
 CC domains, and is necessary for anti-apoptotic activity (by  
 CC similarity). Also interacts with Apaf-1 and RAf-1.  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: alpha (shown here) and beta;  
 CC are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 CC for interaction with RAf-1.  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle. In the absence of  
 CC growth factors, Bcl2 appears to be phosphorylated by other protein  
 CC kinases such as ERKs and stress-activated kinases.  
 CC -1- Dephosphorylated by protein phosphatase 2A (PP2A) (by similarity).  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity.  
 CC -1- DISEASE: Involved in follicular lymphoma (FL) (also known as type  
 CC II chronic lymphatic leukemia) by a chromosomal translocation  
 CC t(14;18)(q32;q21) which involves Bcl2 and immunoglobulin gene  
 CC regions.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;  
 CC WWW="http://www.intoblogen.it/services/chromocancer/Genes/BCL2ID49.html".  
 CC  
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 CC  
 CC -----  
 CC EMBL: M13994; AAS51813.1; ALT\_SEQ.  
 CC EMBL: M13995; AAS51814.1; ALT\_SEQ.  
 CC DR

DR EMBL: M14745; AAS55591.1; -;  
 DR EMBL: X06487; CAA29778.1; -;  
 DR EMBL: S72602; AAD14111.1; ALT\_SEQ.  
 DR PIR: A29409; TVH0A1.  
 DR PIR: B29409; TVH0B1.  
 DR PIR: A24428; TVH0B1.  
 DR PIR: C37332; C37332.  
 DR PIR: D37332; D37332.  
 DR HSSP: Q07817; 1MAZ.  
 DR Genew: HGNC:990; BCL2.  
 DR MIM: 151430; -;  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH4.  
 DR InterPro: IPR004725; BCL2\_Treg.  
 DR Pfam: PF00452; BCL-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMS: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS00652; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4.1; 1.  
 DR PROSITE: PS01260; BH4.1; 1.  
 DR PROSITE: PS0063; BH4.2; 1.  
 KW Proto-oncogene: Apoptosis; Bcl2; 1.  
 KW Mitochondrion; Phosphorylation; Transmembrane;  
 KW Polymorphism; Disease mutation;  
 FT FT DOMAIN 10 30  
 FT FT DOMAIN 93 107  
 FT FT DOMAIN 136 155  
 FT FT DOMAIN 187 202  
 FT FT TRANSMEM 212 233  
 FT FT SITE 34 35  
 FT FT MOD\_RES 70 70  
 FT FT VARSPLIT 196 239  
 FT FT VARIANT 7 7  
 FT FT VARIANT 59 59  
 FT FT VARIANT 93 93  
 FT FT MUTAGEN 34 34  
 FT FT MUTAGEN 64 64  
 FT FT MUTAGEN 145 145  
 FT FT MUTAGEN 188 188  
 FT FT CONFLICT 48 48  
 FT FT CONFLICT 59 59  
 FT FT CONFLICT 117 117  
 FT FT CONFLICT 129 129  
 SQ SEQUENCE 239 AA; 26266 MW; 3C49F2B714DC9CBB CRC64;  
 Query Match 15.0%; Score 133; DB 1; Length 239;  
 Best Local Similarity 19.4%; Pred. No. 7; Ie-06;  
 Matches 40; Conservative 26; Mismatches 52; Indels 88; Gaps 4;  
 QY 37 EYVHRLIRAGLSW-----SAPERASPAG----- 61  
 DB 17 KTIHKLSRGTEWDAVGDAIPGAAPAPGILFSSQPGHTPPAASRDVARTSPLOTDA 76  
 QY 62 -----GRLAECTV 70  
 DB 77 APCAAGPALSPVPVHLLRQAGDDFSRRRRDFAEWSOLHLTPFTARGRFATVVE 136  
 QY 71 LRLGITGCKVYSLSAAGLAVDCVROQAPAMVHALVDCLEFPRKTLATLRRRGVFT 130  
 DB 137 LFRDGVNMGRIVAFFEPGVCVCESVNREMSPLVDNIALMTEYINRHLHTWIDQGWMD 196

QY 131 DVLKCV-VSTKPGFRSHWL-VATLCS 154  
 Db 197 AFVELYGPMSRPLDFFSWLSTKLLS 222

RESULT 3  
 BCL2\_BOVIN STANDARD; PRT; 229 AA.

ID BCL2\_BOVIN STANDARD; PRT; 229 AA.  
 AC 002718;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Holstein; TISSUE=Thymus;  
 RA Reyes R.A., Cockrell G.L.;  
 RT "Bovine leukemia virus associated leukemogenesis is correlated  
 with suppression of programmed cell death and increased expression  
 of Bcl-2."  
 RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 permeability. Appears to function in a feedback loop system with  
 caspases. Inhibits caspase activity either by preventing the  
 release of cytochrome c from the mitochondria and/or by binding to  
 the apoptosis-activating factor (Apaf-1) (By similarity).  
 CC SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 Bcl-x(L). Heterodimerization with BAX requires intact BHL and BH2  
 domains, and is necessary for anti-apoptotic activity (By  
 similarity). Also interacts with Apaf-1 and RAIF-1 (By similarity).  
 CC SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 membrane of the nuclear envelope and the endoplasmic reticulum (By  
 similarity).  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 for interaction with RAIF-1 (By similarity).  
 CC -1- PPM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 on Ser-70 by PKC is required for the anti-apoptosis activity and  
 occurs during the G2/M phase of the cell cycle (By similarity). In  
 the absence of growth factors, Bcl2 appears to be phosphorylated  
 by other protein kinases such as ERKs and stress-activated  
 kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By  
 similarity).  
 CC -1- PPM: Proteolytically cleaved by caspases during apoptosis. The  
 cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 activity, causes the release of cytochrome c into the cytosol  
 promoting further caspase activity (By similarity).  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: U92434; AAB53319.1; -  
 CC HSSP: Q07817; 1MAZ  
 CC InterPro: IPR002475; BCL2\_family.

DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH4.  
 DR InterPro: IPR004725; BCL2\_Reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00285; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
 FT DOMAIN 10 68  
 FT DOMAIN 64 68  
 FT DOMAIN 69 72  
 FT DOMAIN 83 97  
 FT DOMAIN 126 145  
 FT DOMAIN 177 192  
 FT TRANSMEM 202 223  
 FT SITE 34 35  
 FT MOD\_RES 63 63  
 SO SEQUENCE 229 AA; 2509 MW; ADIDDAF98FFIID CRC64;  
 Query Match 14.9%; Score 132; DB 1; Length 229;  
 Best Local Similarity 19.7%; Pred. No. 8.4e-06;  
 Matches 41; Conservative 26; Mismatches 55; Indels 86; Gaps 4;  
 QY 37 EYVARLRRLRLSLW-----SAPERASAPG----- 61  
 Db 17 KYIHKLQSRQYEWADGAGAPGAAPAGILSSQGRTPAPRTSPPPAAAGAP 76  
 QY 62 -----GRLEACTVLLRLGITWGK 80  
 Db 77 SPVPPVHLTLRQAGDDPSRRYRDFAEMSSQLHTPTAREERATVEELFROGVMMGR 136  
 QY 81 VSLYSAAAGLAVDCVROAPAMVHALVDCGEFVRKTLATWLRRGWDVLCV-VST 139  
 Db 137 IVAFEEFGVCVCSVSNREMSPLVDISALMWTETLRLHTLTIODNGDAFVELYGPSM 196  
 QY 140 KPGFRSHWLVAITLCSFGHFLKAAFFLL 167  
 Db 197 RPLDFSWL-----SLKALLSLAL 215  
 RESULT 4  
 BCL2\_CRILLO STANDARD; PRT; 236 AA.  
 ID BCL2\_CRILLO STANDARD; PRT; 236 AA.  
 AC Q9JUV8;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2.  
 OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetulus.  
 OC NCBI\_TaxID=10030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=20431763; Pubmed=10973819;  
 RA Tomicic M.T., Christmann M., Kaina B.;  
 RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2  
 protein."  
 RL Biochem. Biophys. Res. Commun. 275:899-903(2000).  
 RL [2]  
 RP SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES.  
 RX MEDLINE=21092839; Pubmed=11101062;  
 RA Tomicic M.T., Kaina B.;

RT "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9 and caspase-3.";  
 RL Biochem. Biophys. Res. Commun. 281:408(2001).  
 CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (APAF-1) (By similarity).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(L). Heterodimerization with BAX requires intact BHL and BH2  
 CC domains, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with APAF-1 and RAf-1 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 CC for interaction with RAf-1 (By similarity).  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle (By similarity). In  
 CC the absence of growth factors, Bcl2 appears to be phosphorylated  
 CC by other protein kinases such as ERKs and stress-activated kinases  
 CC (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A)  
 CC (By similarity).  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BHL) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC  
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 CC  
 CC EMBL: AJ271720; CAB92245.1; -  
 CC HSSP: Q07817; IMAZ.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH4.  
 DR InterPro: IPR004725; BCL2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM0265; BH4; 1.  
 DR TIGRfams: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS01260; BH4\_2; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
 FT DOMAIN 10 30 BH4.  
 FT DOMAIN 90 104 BH1.  
 FT DOMAIN 133 152 BH2.  
 FT DOMAIN 184 199 BH3.  
 FT DOMAIN 209 230 POTENTIAL.  
 FT STRANSMEM 64 65 CLEAVAGE (BY CASPASE-3 AND CASPASE-9).  
 FT SITE 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
 FT MOD\_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
 FT SEQUENCE 236 AA; 26491 MW; BECADFLEF337228 CRC64;  
 Query Match 14.8%; Score 131; DB 1; Length 236;  
 Best Local Similarity 19.6%; Pred. No. 1.1e-05;

Matches 43; Conservative 27; Mismatches 57; Indels 92; Gaps 5;  
 QY 28 VAQAKALG-----REYHARLLRAGLSW-----SAPERRSPAG----- 61  
 Db 1 MAQAGRTGIDNRRTWKYTHKLSQKGYENDVDVDAAPGAPFGIRFSFQESNPTPA 60  
 QY 62 ----- 61  
 Db 61 VHRDMAFRTSPLRPVATGPTLSPVPVHLLRRAGDPSRRYRDEAFEMSQHLHP 120  
 QY 62 ----GLAEVCYVLLGLITWKVSLYSNAGLAVDCYRQAPAMVHALVDCGFEVVK 117  
 Db 121 FTARGFAFVVELEFDGVMNGRIVAFEPFGGVCSVNRKMSPLVDNIALMTEYLNR 180  
 QY 118 TLATWLRRRGGWTDVLCV-VSKPGFRSHL-VATLCS 154  
 Db 181 HLHTWIQDNGMDAFVELYGPVRLPFDPSWLSKTLIS 219  
 RESULT 5  
 BCL2\_MOUSE  
 ID BCL2\_MOUSE STANDARD; PRT; 236 AA.  
 AC P10417; P10418;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2 OR BCL-2.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_Taxid:10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RC STRAIN-BALB/C; TISSUE=Liver;  
 RX MEDLINE=87187643; PubMed=3032455;  
 RA Negini M., Slini E., Kozak C., Tsujimoto Y., Croce C.M.;  
 RT "Molecular analysis of mbcl-2: structure and expression of the murine  
 RT gene homologous to the human gene involved in follicular lymphoma.";  
 RT Cell 49:455-463(1987).  
 RN [2]  
 RP REVISIONS TO 221-222.  
 RX MEDLINE=9235724; PubMed=1508712;  
 RA Eguchi Y., Ewert D.L., Tsujimoto Y.;  
 RT "Isolation and characterization of the chicken bcl-2 gene: expression  
 RT in a variety of tissues including lymphoid and neuronal organs in  
 RT adult and embryo.";  
 RT Nucleic Acids Res. 20:4187-4192(1992).  
 RN [3]  
 RP PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.  
 RX MEDLINE=97277291; PubMed=9115213;  
 RA Ito T., Deng X., Carr B., May W.S. Jr.;  
 RT "Bcl-2 phosphorylation regulated for anti-apoptosis function.";  
 RT J. Biol. Chem. 272:11671-11673(1997).  
 RN [4]  
 RP DEPHOSPHORYLATION BY PP2A.  
 RX MEDLINE=99069407; PubMed=9852076;  
 RA Deng X., Ito T., Carr B., Mummy M., May W.S. Jr.;  
 RT "Reversible phosphorylation of bcl2 following interleukin 3 or  
 RT bryostatin 1 is mediated by direct interaction with protein  
 RT phosphatase 2A\*.";  
 RT J. Biol. Chem. 273:34157-34163(1998).  
 RL -1- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (APAF-1).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(L). Heterodimerization with BAX requires intact BHL and BH2  
 CC domains, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with APAF-1 and RAf-1.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BHL) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC  
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 CC  
 CC EMBL: AJ271720; CAB92245.1; -  
 CC HSSP: Q07817; IMAZ.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH4.  
 DR InterPro: IPR004725; BCL2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM0265; BH4; 1.  
 DR TIGRfams: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS01260; BH4\_2; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
 FT DOMAIN 10 30 BH4.  
 FT DOMAIN 90 104 BH1.  
 FT DOMAIN 133 152 BH2.  
 FT DOMAIN 184 199 BH3.  
 FT DOMAIN 209 230 POTENTIAL.  
 FT STRANSMEM 64 65 CLEAVAGE (BY CASPASE-3 AND CASPASE-9).  
 FT SITE 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
 FT MOD\_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
 FT SEQUENCE 236 AA; 26491 MW; BECADFLEF337228 CRC64;  
 Query Match 14.8%; Score 131; DB 1; Length 236;  
 Best Local Similarity 19.6%; Pred. No. 1.1e-05;

```

CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -1- ALTERATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;
CC are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAf-1.
CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle. In the absence of
CC growth factors, Bcl2 appears to be phosphorylated by other protein
CC kinases such as ERKs and stress-activated kinases.
CC Dephosphorylated by protein phosphatase 2A (PP2A).
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@1sb-sib.ch).
CC -----
DR EMBL, L31532; AAA37282.1; -.
DR EMBL, M16506; AAA37282.1; JOINED.
DR EMBL, M16506; AAA37281.1; -.
DR PIR, A25960; TVMSA1.
DR PIR, B25960; TVMSB1.
DR PIR, E37332; E37332.
DR HSSP, Q07817; 1MAZ.
DR MGD, MGI:88138; Bcl2.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR003093; Bcl2_BH.
DR InterPro: IPR004725; Bcl2_reg.
DR Pfam, PF00452; Bcl-2; 1.
DR Pfam, PF02180; BH4; 1.
DR SMART, SM00337; BCL; 1.
DR SMART, SM00265; BH4; 1.
DR TIGRFAMs, TIGR00865; bcl-2; 1.
DR PROSITE, PSS0062; BCL2_FAMILY; 1.
DR PROSITE, PS01080; BH1; 1.
DR PROSITE, PS01258; BH2; 1.
DR PROSITE, PS01259; BH3; 1.
DR PROSITE, PS01260; BH4_1; 1.
DR PROSITE, PSS0063; BH4_2; 1.
DR Apoptosis: Alternative splicing; Transmembrane; Mitochondrion;
KM phosphorylation.
KW DOMAIN.
FT DOMAIN 10 30 BH4.
FT DOMAIN 90 104 BH3.
FT DOMAIN 133 152 BH1.
FT DOMAIN 184 199 BH2.
FT TRANSMEM 209 230 POTENTIAL.
FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT MOD_RES 70 70 PHOSPHORYLATION (BY PKC).
FT VARSPIC 193 236 DAFVELGPMRPLFDFSWLSLKLTLALVGCITLGAAYL
FT VARSPLIC 193 236 GHK -> VGACTIVE (IN ISOFORM BETA).
SO SEQUENCE 236 AA; 26425 MW; AA85EF6B0766BEDA CRC64;
Query Match 14.78; Score 130; DB 1; Length 236;
Best Local Similarity 19.66; Pred. No. 1,4e-05;
Matches 43; Conservative 27; Mismatches 57; Indels 92; Gaps 5;
OY 28 VAAQKALG-----REYVHARLLRAGLSW-----SAPERASAPAP----- 61

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DB 1 MAQAGRTGYDNRREIVKRYIHYKLSQGYEMDAGDADAPLAAPPGJFSFQSPSPMPA 60
OY 62 ----- 61
DB 61 VIREMAARTSPRLPVAAGPALSPVPCVHLTLRRAGDDPSRRYRDPFAEMSSOLHLP 120
OY 62 -----GRLEAVCTVLLRLGITWGVSLYSAAAGLAVDCVQAQAPMAVHALVDCLEFVRK 117
DB 121 FTAREAFATVVEELPRDGVNMGRIYAFEEFGVYKGVESVNMESPLVONIALMTEYINR 180
OY 118 TLATLRRRGWTDVLCV-VSTKPFRRSHL-VATLCS 154
DB 181 HLHTWIDQNGMDAFVELYGPMSRPLFDFSWLSLKLTL 219
RESULT 6
BCL2_CHICK STANDARD; PRT; 233 AA.
AC Q00709;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2 OR BCL-2.
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92375724; PubMed=1508712;
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT "Isolation and characterization of the chicken bcl-2 gene: expression
RT in a variety of tissues including lymphoid and neuronal organs in
RT adult and embryo."
RL Nucleic Acids Res. 20:4187-4192(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=B-cell lymphoma;
RX MEDLINE=92379084; PubMed=1511008;
RA Cazalis-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;
RT "Molecular cloning and DNA sequence analysis of cDNA encoding chicken
RT Bcl-2."
RL Biochem. Biophys. Acta 1132:109-113(1992).
CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1).
CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity (By
CC similarity). Also interacts with APAF-1 and RAf-1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -1- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen,
CC kidney, heart, ovary and brain, with the highest levels in the
CC thymus. In the embryo, highly levels expressed in all tissues with
CC high levels in the bursa of Fabricius.
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAf-1 (By similarity).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
DR EMBL; D11382; BAA01978.1; -  
DR EMBL; D11381; BAA01978.1; JOINED.  
DR EMBL; 211961; CAA78018.1; -  
DR PIR; A37332; A37332.  
DR PIR; S24390; S24390.  
DR HSP; Q07817; IMAZ.  
DR InterPro; IPR002475; BCL2\_family.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR004725; Bcl2\_Reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
DR Apoptosis; Transmembrane; Mitochondrion.  
KW DOMAIN 10 30 BH4.  
FT DOMAIN 87 101 BH3.  
FT DOMAIN 130 149 BH1.  
FT DOMAIN 181 196 BH2.  
FT TRANSMEM 208 228 POTENTIAL.  
FT CONFLICT 64 64 E -> S (IN REF. 2).  
FT CONFLICT 67 82 GSAASEVPPAEGLRP -> ARLLVRCPLRGCA  
(IN REF. 2).  
FT CONFLICT 121 121 H -> T (IN REF. 2).  
FT CONFLICT 139 139 G -> V (IN REF. 2).  
SQ SEQUENCE 233 AA; 25687 MW; 5252555ACB6AC3D CRC64;

Query Match 13.1%; Score 115.5; DB 1; Length 233;  
Best Local Similarity 16.4%; Pred. No. 0.00035;  
Matches 35; Conservative 26; Mismatches 62; Indels 91; Gaps 3;

QY 37 EYVHARLRLAGLSWSPAPRASPAP----- 60  
DB 17 KYIHKLSQRYDWAAGDRPVPAPAPAAVAAGASSHHRRPPGSAASEVPP 76  
QY 61 -----GRLAEVCTYLLRLGI 76  
DB 77 AEGLRPAPGVHALLRQAGDEFRRYQDFQMSQGLHLPFTAHGREFVAVEELFRDGV 136  
QY 77 TWGKVSLSYSAAGLAVDCVRAQAPAMVHALVDCLEFVRKTLATWLRRRGGWTDVLCV 136  
DB 137 NWGRIVAFEEGGVACVSVNREMSPLVDNATWTEYTLNRLHNLHNIODNGMDAIVELY 196  
QY 137 -VSTKPGFRSHM-----LVATLCSFGRFL 159  
DB 197 GNSMRPLDFSMISLKITLSLVVGACITLGAYL 230

## RESULT 7

ARL\_XENLA  
ID ARL\_XENLA STANDARD; PRT; 228 AA.  
AC 091827;  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptosis regulator R1 (XRL) (Fragment).  
OS Xenopus laevis (African clawed frog).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
CC Xenopodinae; Xenopus.

OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RX MEDLINE=95331613; PubMed=7607538;  
RA Cruz-Reyes J., Tata J.R.;  
RT "Cloning, characterization and expression of two Xenopus bcl-2-like  
cell-survival genes.";  
RL Gene 158:171-179(1995).

CC -1- SUBCELLULAR LOCATION: Membrane-bound (potential).  
CC -1- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE  
CC BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND  
CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; X82462; CAA57845.1; -  
DR HSP; Q07817; IMAZ.  
DR InterPro; IPR002475; BCL2\_family.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR Apoptosis; Transmembrane.  
KW NON\_TER 1 1  
FT DOMAIN 120 139 BH1.  
FT DOMAIN 171 186 BH2.  
FT TRANSMEM 207 227 POTENTIAL.  
SQ SEQUENCE 228 AA; 25068 MW; C499D49A585F8A9 CRC64;

Query Match 12.7%; Score 112.5; DB 1; Length 228;  
Best Local Similarity 21.3%; Pred. No. 0.00066;  
Matches 33; Conservative 27; Mismatches 52; Indels 43; Gaps 4;

QY 19 DRWPTDKELVAVQ---AKALGREYVHARLRLAGLSWSPAPRASPAP----- 59  
DB 32 DKYLFEGQWMAQSDGSRALYEDLVRYKLCQSL---VPEPSGAASCLHSMRAAGDEF 88  
QY 60 -----PG-----GRLAEVCTYLLRLGITWGVLSYSAAGLAVDCVRQ 98  
DB 89 EERFROAFSEISTQIHVHPGTAAYARFAEYVAGSLFQGVNMGRIVAFVFGAALCAESYVK 148  
QY 99 AQPAVHALVDCLEFVRKTLATWLRRRGGWTDVLCV 133  
DB 149 EMSPLPRIQDMWYTYLETNLRDWIOSNGMNGFL 183

## RESULT 8

BCLX\_CHICK  
ID BCLX\_CHICK STANDARD; PRT; 229 AA.  
AC 007816; 098908;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Apoptosis regulator Bcl-X.  
GN BCL2L1 OR BCLX OR BCL-X.  
OS Gallus gallus (Chicken).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;





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FT  VARSP.LIC 194 233 -LYGNNAASESKSGGERNRNRLTGMATAGVLLGSLPSRK
FT  FT  -> GHDCGWSGASLTLTQSEVTRH (IN ISOFORM BCL-
SQ  SEQUENCE 233 AA; 26132 MW; 24D2AC79887E072E CRC64;
      X(DELTA-TM)).
Query Match 11.8% Score 104; DB 1; Length 233;
Matches 17; Conservative 15; Mismatches 32; Indels 0; Gaps 0;
QY 66 ECVTLVRLGLTGWKRVSLYSAAAGLAVDCVROAPAMVHALVDCIGEFVKRTLATWLR 125
Db 125 QVAMELFRPDGYNMGRIYAFSEFGALTCESYSDKENVLYSRMIAISMATYLVNDHLEPWQ 184
QY 126 RGVW 129
Db 185 NGWV 188

RESULT 10
BCLX_RAT STANDARD; PRT; 233 AA.
ID BC1X_RAT
AC P53563; Q62678; P70614; P70613; Q62836; Q64087; Q64128;
PT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-x.
DE BCL2L1 OR BCL2L OR BCLX.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RA TISSUE=Brain;
RC Michaelidis T.M.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RC Wesselingh S.L.; David G.L.; Choi S.; Veluona M.; Hardwick J.M.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
RA TISSUE=Thymus;
RC MEDLINE=96278736; PubMed=8662675;
RA Shiraawa N.; Inohara N.; Okada S.; Yuzaki M.; Shoji S.-I.; Ohta S.;
RL "An additional form of rat Bcl-x, Bcl-xbeta, generated by an
RT unspliced RNM, promotes apoptosis in promyeloid cells.";
RL J. Biol. Chem. 271:13258-13265(1996).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RA STRAIN=Sprague-Dawley; TISSUE=Ovary;
RC MEDLINE=95129487; PubMed=7828336;
RA Tilly J.L.; Tilly K.I.; Kenton M.L.; Johnson A.L.;
RT "Expression of members of the bcl-2 gene family in the immature rat
RA ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT cell apoptosis is associated with decreased bax and constitutive
RL bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
RL Endocrinology 136:232-241(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RA MEDLINE=98010630; PubMed=9346936;
RA Artioni M.; Kunishima N.; Inohara N.; Ishibashi Y.; Ohta S.;
RA Morikawa K.;
RT "Crystal structure of rat Bcl-xL. Implications for the function of
RT the Bcl-2 protein family.";
RL J. Biol. Chem. 272:27886-27892(1997).
CC 1-1 FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC caspases (By similarity). Appears to regulate cell death by
CC blocking the voltage-dependent anion channel (VDAC) by binding
CC to it and preventing the release of the caspase activator,
CC cytochrome c, from the mitochondrial membrane. The Bcl-x(S) and
CC Bcl-x(beta) isoforms promote apoptosis.

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CC	-1	SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By similarity).	
CC	-1	similarity. Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity).	
CC	-1	SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE (By similarity).	
CC	-1	ALTERNATIVE PRODUCTS: 3 ISOFORMS: BCL-X(L) (SHOWN HERE), BCL-X(S) AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.	
CC	-1	TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT DETECTABLE LEVEL OF BCL-X(S).	
CC	-1	DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bcl2 family members and for repression of cell death.	
CC	-1	PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity (By similarity).	
CC	-1	SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.	
CC	-1	SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.	
CC	-1	SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.	
CC	-1	SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.	
CC	-1	SIMILARITY: BELONGS TO THE BCL-2 FAMILY.	
CC		-----	
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CC		or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	
DR	EMBL:	X82537; CAAS7886.1; -	
DR	EMBL:	X82537; CAAS7887.1; -	
DR	EMBL:	U10579; AAA19257.1; -	
DR	EMBL:	U72350; AAB17353.1; -	
DR	EMBL:	U72349; AAB17352.1; -	
DR	EMBL:	U34963; AAA7686.1; -	
DR	EMBL:	S76513; AAC60701.1; ALT_INIT.	
DR	EMBL:	S78284; AAC60702.1; -	
DR	PDB:	1AF3; 07-JUL-97.	
DR	InterPro:	IPR002475; BCL2_family.	
DR	InterPro:	IPR000712; Bcl2_BH.	
DR	InterPro:	IPR003093; Bcl2_BH4.	
DR	InterPro:	IPR004725; Bcl2_reg.	
DR	Pfam:	PF00452; Bcl-2; 1.	
DR	Pfam:	PF02180; BH4; 1.	
DR	SMART:	SM00337; BCL; 1.	
DR	SMART:	SM00265; BH4; 1.	
DR	TIGRFAMS:	TIGR00865; bcl-2; 1.	
DR	PROSITE:	PS50062; BCL2_FAMILY; 1.	
DR	PROSITE:	PS01080; BH1; 1.	
DR	PROSITE:	PS01258; BH2; 1.	
DR	PROSITE:	PS01259; BH3; 1.	
DR	PROSITE:	PS01260; BH4_1; 1.	
DR	PROSITE:	PS50063; BH4_2; 1.	
KW	Apoptosis; Mitochondrion; Alternative splicing; Transmembrane; 3D-structure.		
FT	DOMAIN	4	24
FT	DOMAIN	86	100
FT	DOMAIN	129	148
FT	DOMAIN	180	195
FT	TRANSMEM	210	226
FT	VARSPPLIC	126	188
FT	VARSPPLIC	189	233
FT	CONFLICT	6	6
FT	CONFLICT	12	12
FT	CONFLICT	64	64
FT	CONFLICT	81	81
FT	CONFLICT	119	119
FT	CONFLICT	143	144
FT	CONFLICT	199	199
FT	CONFLICT	199	199

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FT CONFLICT 201 201 A->P (IN REF. 4)
SQ SEQUENCE 233 AA; 26158 MW; 2862B6C65864BC6F CRC64;
Query Match 11.8%, Score 104; DB 1; Length 233;
Best Local Similarity 26.6%; Pred. No. 0.0045;
Matches 17; Conservative 15; Mismatches 32; Indels 0; Gaps 0;
QY 66 EVCYTLRLRLGITMGCVVSLYSAAGLAVDCVROQAPPAVHMLVYDCLGSEFVKRTLATWLR 125
DB 125 QVNLPEFDGVMWGRIVAFVSFGALCVESVDKEMQVLSRASMATYLLNDHEPWIOE 184
QY 126 RGGW 129
DB 185 NGGW 188
RESULT 11
BCLX_PIG STANDARD; PRT; 233 AA.
ID BCLX_PIG
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-x.
GN BCL2L1 OR BLC2L OR BCLX.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99171363; PubMed=10072723;
RA Battling B., Hoffmann J., Holtz J., Schulz R., Hensch G., Darmer D.;
RT "Quantification of cardioprotective gene expression in porcine
RT short-term hibernating myocardium.";
RL J. Mol. Cell. Cardiol. 31:147-158(1999).
CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC caspases (By similarity). Appears to regulate cell death by
CC blocking the voltage-dependent anion channel (VDAC) by binding
CC to it and preventing the release of the caspase activator,
CC cytochrome c, from the mitochondrial membrane.
CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC similarity). Heterodimerization with BAX does not seem to be
CC required for anti-apoptotic activity (By similarity).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC ENVELOPE (By similarity).
CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization
CC with other Bcl2 family members and for repression of cell death.
CC -1- PTM: Proteolytically cleaved by caspases during apoptosis (By
CC similarity). The cleaved protein, lacking the BH4 domain, has pro-
CC apoptotic activity (By similarity).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC
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CC
DR EMBL; AJ001203; CAA04597.1; -
DR HSSP; Q07817; IMAZ.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.

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DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRfam: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1.  
 DR PROSITE: PS0063; BH4\_2; 1.  
 DR Apoptosis; Mitochondrion; Transmembrane.  
 KW DOMAIN 4 24 BH4.  
 FT DOMAIN 8 100 BH3.  
 FT DOMAIN 129 148 BH1.  
 FT DOMAIN 180 195 BH2.  
 FT TRANSMEM 210 226 POTENTIAL.  
 SQ SEQUENCE 233 AA; 26061 MW; 18BF6FA0441912B2 CRC64;  
 Query Match 11.7%; Score 103; DB 1; Length 233;  
 Best Local Similarity 26.6%; Pred. No. 0.0057;  
 Matches 17; Conservative 15; Mismatches 32; Indels 0; Gaps 0;  
 QY 66 EVCYLLRLRGTWGVSVISXSAAGLAVDCVQAPAMVHALVDCLGFEVKTATWLR 125  
 DB 125 QVLNLEFRDGVNMGRIVAFFSGALCVESVDKEMQVLVSRITATWATYLNHLEPWIOE 184  
 QY 126 RCGM 129  
 DB 185 NCGM 188  
 RESULT 12  
 BCLX\_HUMAN STANDARD: PRT; 233 AA.  
 AC 007817; 092976;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-x.  
 GN BCL2L1 OR BCL2L OR BCLX.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM X(L) AND X(S)).  
 RX Bojse L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,  
 RA Turka L.A., Mao X., Nunez G., Thompson C.B.,  
 RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator  
 of apoptotic cell death.";  
 RL Cell 74:597-608(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM BETA).  
 RA Inohara N., Ohta S.,  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.  
 RX MEDLINE=95372373; PubMed=7644501;  
 RA Sedlak T.W., Olivai Z.N., Yang E., Wang K., Bojse L.H., Thompson C.B.,  
 RA Korsmeyer S.J.,  
 RT "Multiple Bcl-2 family members demonstrate selective dimerizations  
 with Bax.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).  
 RN [4]  
 RP MUTAGENESIS OF BHL AND BH2 DOMAINS.  
 RX MEDLINE=96170038; PubMed=8596636;  
 RA Cheng E.H.-Y., Levine B., Bojse L.H., Thompson C.B., Hardwick J.M.,  
 RA Korsmeyer S.J.,  
 RT "Bax-independent inhibition of apoptosis by Bcl-XL.";  
 RL Nature 379:554-556(1996).  
 RN [5]  
 RP STRUCTURE BY NMR OF 1-209.

RX MEDLINE=97172562; PubMed=9020082;  
 RA Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E.,  
 RA Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,  
 RA Thompson C.B., Fesik S.W.,  
 RT "Structure of Bcl-XL-Bak peptide complex: recognition between  
 RT regulators of apoptosis.";  
 RL Science 275:983-986(1997).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.  
 RX MEDLINE=96256675; PubMed=8692274;  
 RA Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,  
 RA Yoon H.S., Nettesheim D., Chang B.S., Thompson C.B., Wong S.L.,  
 RA Ng S.L., Fesik S.W.,  
 RT "X-ray and NMR structure of human Bcl-XL, an inhibitor of programmed  
 RT cell death.";  
 RL Nature 381:335-341(1996).  
 RN [7]  
 RP CLEAVAGE BY CASPASES, AND MUTAGENESIS OF ASP-61.  
 RX MEDLINE=98118550; PubMed=9435230;  
 RA Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.,  
 RA Takahashi A., Kastan M.B., Griffin D.E., Earnshaw W.C., Velluona M.A.,  
 RA Hardwick J.M.,  
 RT "Modulation of cell death by Bcl-XL through caspase interaction.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).  
 CC -1- FUNCTION: Potent inhibitor of cell death. Inhibits activation of  
 CC caspases (By similarity). Appears to regulate cell death by  
 CC blocking the voltage-dependent anion channel (VDAC) by binding  
 CC to it and preventing the release of the caspase activator,  
 CC cytochrome c, from the mitochondrial membrane. The Bcl-x(S)  
 CC isoform promotes apoptosis.  
 CC -1- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2.  
 CC Heterodimerization with BAX does not seem to be required for anti-  
 CC apoptotic activity.  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
 CC ENVELOPE (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: BCL-X(L) (SHOWN HERE), BCL-X(S)  
 CC AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS  
 CC THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING  
 CC LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING  
 CC LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
 CC The BH1 and BH2 domains are required for both heterodimerization  
 CC with other Bcl2 family members and for repression of cell death.  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; 223116; CAA80662.1; -;  
 CC EMBL; 223115; CAA80661.1; -;  
 CC EMBL; 072398; AAB17354.1; -;  
 CC PDB; 1BXL; 29-OCT-97;  
 CC PDB; 1LXL; 21-APR-97;  
 CC PDB; 1MAZ; 21-APR-97;  
 CC Genew; HGNC:992; BCL2L1.  
 CC MIM; 600039; -;  
 CC InterPro; IPR002475; BCL2 family.  
 CC InterPro; IPR000712; Bcl2\_BH.  
 CC InterPro; IPR003093; Bcl2\_BH4.  
 CC InterPro; IPR004725; Bcl2\_reg.

DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; Bcl-1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;  
 KM 3D-structure.  
 FT DOMAIN 4 24 BH4.  
 FT DOMAIN 86 100 BH3.  
 FT DOMAIN 129 148 BH1.  
 FT DOMAIN 180 195 BH2.  
 FT TRANSMEM 210 226 POTENTIAL.  
 FT SITE 61 61 CLEAVAGE BY CASPASE-1.  
 FT VARSPLIC 126 188 MISSING (IN ISOFORM BCL-X(S)).  
 FT VARSPLIC 189 233 DTFVELGNMAAESRKGQERNFMFLGTMVAVAGVILGSL  
 FT FSRK -> VTRKPLVCFPSLASGQSRPTALLLYFLLCWVI  
 FT VGDVDS (IN ISOFORM BCL-X(BETA)).  
 FT D->A: NO CLEAVAGE BY CASPASE-1 NOR BY  
 FT CASPASE-3.  
 FT FRD->VRA: NO HETERODIMERIZATION WITH BAX.  
 FT VNM->AIL: LOSS OF ANTI-APOPTOTIC  
 FT ACTIVITY.  
 FT GRI->ELN: LOSS OF ANTI-APOPTOTIC  
 FT ACTIVITY.  
 FT MUTAGEN 138 140 ACTIVITY.  
 FT MUTAGEN 138 138 G->A: NO HETERODIMERIZATION WITH BAX.  
 FT MUTAGEN 148 148 G->E: NO HETERODIMERIZATION WITH BAX.  
 FT MUTAGEN 156 156 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT MUTAGEN 176 176 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT MUTAGEN 188 189 WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY  
 FT BY ABOUT HALF.  
 FT MUTAGEN 189 189 D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.  
 FT CONFLICT 70 70 G->A (IN REF. 1; CAA80661).  
 FT SEQUENCE 233 AA; 26049 MW; E09D3CDD851AE9BE CRC64;  
 SO  
 Query Match 11.5%; Score 102; DB 1; Length 233;  
 Best Local Similarity 26.6%; Pred. No. 0.0071;  
 Matches 17; Conservative 15; Mismatches 32; Indels 0; Gaps 0;  
 Oy 66 EVCYVLRGLGTTGWKVSLSYSAAGLAVDCYRQAPAVHALVDCLGFEVKTATWIR 125  
 Db 125 QVVELFDFGVNMGRIYAFSEFGALCVESVDKEMQVLSRIAAMATYIINDHLEPWIOE 184  
 Oy 126 RGGW 129  
 Db 185 NGW 188  
 RESULT 13  
 BAXB\_HUMAN STANDARD; PRT; 218 AA.  
 AC 007814;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator BAX, cytoplasmic isoform beta.  
 GN BAX.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN 11;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=B-cell;  
 RX MEDLINE=93364978; PubMed=8358790;  
 RA Oliva L Z N., Millman C L., Korsmeyer S J.;  
 RT "bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that  
 accelerates programmed cell death.";

RL Cell 74:609-619(1993).  
 CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND  
 CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS  
 CC HOMOLOG E1B 19K PROTEIN.  
 CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,  
 CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE  
 CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY  
 CC ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  
 CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND  
 CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION  
 CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: L22474; AAA03620.1; -  
 DR PIR: B47538; B47538.  
 DR HSSP: Q07817; IMAZ.  
 DR GeneW: HGNC:959; BAX.  
 DR MIM: 600040; -  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BCL2\_FAMILY; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 KW Apoptosis; Alternative splicing  
 FT DOMAIN 59 73 BH3.  
 FT DOMAIN 98 118 BH1.  
 FT DOMAIN 150 165 BH2.  
 FT SEQUENCE 218 AA; 24220 MW; F69DCD70F960192AF CRC64;  
 SO  
 Query Match 11.3%; Score 100; DB 1; Length 218;  
 Best Local Similarity 22.2%; Pred. No. 0.01;  
 Matches 34; Conservative 25; Mismatches 52; Indels 42; Gaps 5;  
 Oy 22 PTDKELVAQAKALGRE-YVHARLLRAGLSWSAPER-SPAP-GGRLAEVCTVLRG-- 75  
 Db 13 PTSSQIMKGTGALLQGIQDRAGRMG--GEAPELADLPVPODASTKLSCLKRIGDEL 70  
 Oy 76 -----ITWGVVSLYSAAAGLAVDCYRQAP 101  
 Db 71 DSNMELQRIAAVDTPDSREVEFFRYAADMFSQDNFMGRVVALFFPAKSLVLAALCTKVP 130  
 Oy 102 AMVHALVDCLGFEVKTATWIRRGWTDVLR 134  
 Db 131 ELIRITMGWTDPLERLRLGHIQDGGVNRLLK 163  
 RESULT 14  
 BCLW\_MOUSE STANDARD; PRT; 193 AA.  
 AC P70345;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-W.  
 GN BCL2L2 OR BCLW.

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358615; PubMed-8761287;
RA Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Johnson N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
RL "bc1w", a novel member of the bcl-2 family, promotes cell survival.";
Oncogene 13:665-675(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=C57BL/10J;
RA Russell A.J., Mayme K.G., Moss J.E., Parlow A.F., Skinner M.K.,
RA Russel L.D., Macgregor G.R.;
RT "testicular degeneration in bc1w-deficient mice.";
RL Nat. Genet. 18:251-256(1998).
CC -1- FUNCTION: PROMOTES CELL SURVIVAL.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND
IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,
AND SALIVARY GLAND.
CC -1- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
FUNCTION.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL: U59746; AAB09056.1; -
DR EMBL: AF030769; AAB86430.1; -
DR HSSP: Q07817; IMAZ.
DR MGJ: MG1:108052; BCL2I12.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR003093; BCL2_BH4.
DR Pfam: PF00452; BCL-2; 1.
DR Pfam: PF02180; BH4; 1.
DR SMART: SM00337; BCL; 1.
DR SMART: SM00265; BH4; 1.
DR PROSITE: PSS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01260; BH4_1; 1.
DR PROSITE: PSS0063; BH4_2; 1.
DR Apoptosis.
KM FT 9 BH4.
FT 85 BH1.
FT 136 BH2.
SQ DOMAIN 136 151
SQ SEQUENCE 193 AA; 20790 MW; 36CA185F5945DFB4 CRC64;

Query Match 11.2%; Score 99; DB 1; Length 193;
Best local similarity 24.3%; Pred. No. 0.011;
Matches 27; Conservative 19; Mismatches 63; Indels 2; Gaps 2.

QY 22 PTDKELVAQAAGREYUHAIRLRAGLSWASPERASPARG-GRLAEVCTVLRLGITWGK 80
Dd 37 PAADPLHQAMRAAGEDEF-ETRRFRPFSDLAQLHTVTGSAQGQRFTGYVDSELPFGGNMGR 95
Oy 81 VSLYSAAAGLVDCYVRQAQPMAYVALVDLCGEFPRKTATLTALVRRGGTTD 131
Db 96 LVAFVFPAALCAESYNRKEMEPLVGQVDDMWAVLYETRLADIHSNGVAE 146
db 96 LVAFVFPAALCAESYNRKEMEPLVGQVDDMWAVLYETRLADIHSNGVAE 146

```

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RESULT 15
ARL1_XENLA ID ARL1_XENLA STANDARD; PRT; 204 AA.
AC Q91826;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
OE Apoptosis regulator Rlll (XRll).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OX Xenopodinae; Xenopus.
RN NCBI_TaxID=8355;
RP TISSUE FROM N.A.
RX MEDLINE=95331613; PubMed=7607538;
RA Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
   cell-survival genes."
RL Gene 158:171-179(1995).
CC -1- FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -1- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC Tadpoles AND
CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGU 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGU 2 (BH2) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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-----
DR DR EMBL; X82461; CAAS7844.1; -.
DR HSSP; Q07817; IMAZ.
DR InterPro; IPRO02475; BCL2_family.
DR InterPro; IPRO00712; BCL2_BH.
DR InterPro; IPRO03093; BCL2_BH4.
DR InterPro; IPRO04725; BCL2_reg.
DR Pfam; PF00452; BCL-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SMO0337; BCL; 1.
DR SMART; SMO0265; BH4; 1.
DR SMART; TIGR00865; bcl-2; 1.
DR TIGRFAMS; TIGR00865; bcl-2; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
KW Apoptosis; Transmembrane.
FT FT DOMAIN 101 120 BH1.
FT DOMAIN 152 167 BH2.
FT TRANSSEM 181 198 POTENTIAL.
SQ SEQUENCE 204 AA; 23379 MW; 3BFCBBEDDACA03 CRC64;

Query Match 11.1%; Score 98; DB 1; Length 204;
Best Local Similarity 26.6%; Pred. No. 0.015;
Matches 17; Conservative 15; Mismatches 32; Indels 0; Gaps 0;

OY 66 EVCTVLLRLGLTTGQKVVSLYSAAAGLVADVCYRQAOPAMVAHALVDLCIEGFVKTLATMLRR 125
    :||| |||::: | | | | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 97 QVMGLFLFDGNNGWIVAFESFGRALCYESAANKENTDLPLPIYGMNVYLLEHTLDPMNQE 156
OY 126 RGCV 129
    |||
DB 157 NGCW 160
```

Search completed: April 29, 2003, 11:23:57

Thu May 1 13:55:59 2003

us-09-682-667-8.rsp

Page 14

Job time : 6.99217 secs

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GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: April 29, 2003, 11:20:36 ; Search time 10.6527 Seconds  
(without alignments)  
1534.145 Million cell updates/sec

Title: US-09-682-667-8  
Perfect score: 884

Sequence: 1 MEVLRRSSVPAAEIMDAFDR.....TLCSEGRFLKAAPFLUPER 170

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR3:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	15.5	236	2	gene bcl-2 protein
2	133	15.0	239	1	transforming prote
3	131.5	14.9	236	2	BCL-2 - rat (fragm
4	131	14.8	236	1	B-cell lymphoma 2
5	130	14.7	236	1	transforming prote
6	124	14.0	205	1	transforming prote
7	123	13.9	199	1	transforming prote
8	116.5	13.2	216	2	transforming prote
9	115.5	13.1	233	2	transforming prote
10	114	12.9	227	2	apoptosis regulato
11	107	12.1	232	2	transforming prote
12	104.5	11.8	190	2	apoptosis regulato
13	104	11.8	214	2	bcl-2-associated p
14	104	11.8	233	2	bcl-x transmembran
15	104	11.8	233	2	bcl-x long - mouse
16	102	11.5	233	2	BCL-X protein - ra
17	100	11.3	233	2	apoptosis regulato
18	97.5	11.0	233	2	BCL-X-long - rat
19	97	11.0	179	2	Bax-delta protein
20	95	10.7	192	2	bcl-2-associated p
21	95	10.7	211	2	Bak protein - huma
22	93	10.5	133	2	bcl-2-associated p
23	92.5	10.5	143	2	bcl-2-associated p
24	92	10.4	192	2	hemopoietic-specif
25	85.5	9.7	172	2	cdn-2 protein - hu
26	85	9.6	211	2	e antigen precurs
27	84	9.5	212	2	carbamoyl-phosphat
28	83	9.4	1115	2	probable polyketid
29	82	9.3	2126	2	

30	80.5	9.1	2326	2	T29140
31	79.5	9.0	822	2	AE2404
32	79.5	9.0	860	2	C82750
33	78.5	8.9	319	2	T10583
34	78.5	8.9	540	2	T34702
35	78	8.8	183	2	S53181
36	78	8.8	212	2	S25651
37	78	8.8	356	2	G81907
38	78	8.8	419	2	A83133
39	77.5	8.8	154	2	T81894
40	77.5	8.8	364	2	AH1857
41	77.5	8.8	412	2	T37042
42	77.5	8.8	2291	1	A46147
43	77	8.7	175	2	I39055
44	77	8.7	214	2	S47409
45	76.5	8.7	482	2	C86442

## ALIGNMENTS

## RESULT 1

153744 gene bcl-2 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 16-Jul-1999

C:Accession: I53744

R:Sato, T., Irie, S., Krajewski, S., Reed, J.C.

Gene 140, 291-292, 1994

A:Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein:

A:Reference number: I53744; MUID:94193015; PMID:8144041

A:Accession: I53744

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-236 <RES>

A:Cross-references: GB:L14680; NID:9408946; PID:AAA53662.1; PID:9408947

C:Genetics:

A:Gene: bcl-2

C:Superfamily: bcl transforming protein

Query Match	Best Local Similarity	Matches	45; Conservative	25; Mismatches	57; Indels	92; Gaps	5;
OY	28	VQAQALG-----REYVHARLRAGLSW-----SAPERASPAAG-----	11	11	11	11	61
DB	1	MAQAGRTGYDNEIYMKYIHYKLSRGYEMDTGDEDSAPLRAPPGILFSPQESNRTPA	60				60
OY	62	-----					61
DB	61	VHRDFAARTSPRLPVANAGPALSPVPVHLTLRRAGDDFSRRYRDEFAEMSQLHLTP	120				120
OY	62	-----GRLAECVTLRLGITGKVVLSAAGLAVDCYKQAPMVAHLYDCLCEFPYK	117				117
DB	121	FTARGRFATVDELFRRDVGWGMGRIVAFEEFGVGVGNRMSPLVNIALMTMEYINR	180				180
OY	118	TLATVLRRGWTDVLKCY-VSTKPGFRRSHML-VATLCS	154				154
DB	181	HLHTWIDNGMDAFVELYGPMSRPLFDFSWLSTLTLS	219				219

## RESULT 2

TVHUA1 transforming protein bcl-2, splice form alpha - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1988 #sequence\_revision 07-Jun-1996 #text\_change 15-Oct-1999

C:Accession: C37332; A29409; S02452; A24428; A27622; B27622

R:Enguchi, Y., Ewert, D.L., Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a va

A:Reference number: A37332; MUID:9237524; PMID:1508712

A:Accession: C37332

A:Status: nucleic acid sequence not shown; not compared with conceptual translation





Db 181 HLHTWIDNGMDAFVELXGSPVRLPFDPSWLSKTLTLLS 219

RESULT 5

transferring protein bcl-2-alpha - mouse

C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 18-Jun-1999

C:Accession: A25960; E37332  
R:Negishi, M.; Sillini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.

A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homol  
Cell 49, 455-463, 1987

A:Reference number: A90893; MUID:87187643; PMID:3032455

A:Accession: A25960

A:Molecule type: DNA

A:Residues: 1-236 <NEG>  
A:Cross-references: GB:LJ1533; GB:M16506; NID:9468336; PIDN:AAA37282.1; PID:9387109

R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie  
A:Reference number: A37332; MUID:92375724; PMID:1508712

A:Accession: E37332

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: DNA

A:Residues: 1-33,'E','34'-220,'AL','223'-236 <EGU>  
C:Genetics:

A:Gene: BCL2

A:Introns: 192/3

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane pro

Query Match

Best Local Similarity 19.6%; Score 130; DB 1; Length 236;  
Matches 43; Conservative 27; Mismatches 57; Indels 92; Gaps 5;

QY 28 VAQAKALG-----REYVHARLRLAGLSW-----SAPERASPARG----- 61

Db 1 MAQAGRTGYDNRITWKYIHYKLSQRYEMDAGDADAAPLGAAPPTGIFSFQESNPMRA 60

QY 62 ----- 61

Db 61 VHEMAARTSPRLPLVATAGPALSPVPCVHILTLRRAGDDFSRRYRRDFAEMSSQLHLTP 120

QY 62 ----GRLAECYVTLRLGITWGVSLYSAAAGLAVDCYRQAPAMVHALVDCLEGFVRK 117

Db 121 FTARGFATVVEELFRDGVNMGRIYAFEEFGVGVCSYVREMSPLVDNIALMTEYLNR 180

QY 118 TLATWLRGGRGWTDLKCV-VSTKPGFRSHWL-VATLCS 154

Db 181 HLHTWIDNGMDAFVELXGSPVRLPFDPSWLSKTLTLLS 219

RESULT 6

transferring protein bcl-2, splice form beta - human

N:Alternate names: apoptosis regulator bcl-2

C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 15-Oct-1999

C:Accession: B29409; I52566; D37332  
R:Tsujimoto, Y.; Croce, C.M.

Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986

A:Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene  
A:Reference number: A29409; MUID:86259760; PMID:3523487

A:Accession: B29409

A:Molecule type: mRNA

A:Residues: 1-205 <TSU>  
A:Cross-references: GB:M13995; NID:9179368; PIDN:AAA51814.1; PID:9179369

R:Tanaka, S.; Louie, D.C.; Kant, J.A.; Reed, J.C.  
Blood 79, 229-237, 1992

A:Title: Frequent incidence of somatic mutations in translocated BCL2 oncogenes of non-H  
A:Reference number: I52566; MUID:92096610; PMID:1339299

A:Accession: I52566

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-131 <TAN>  
A:Cross-references: GB:S72602; NID:9241046; PIDN:AAD14111.1; PID:94261811

R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a va  
A:Reference number: A37332; MUID:92375724; PMID:1508712

A:Accession: D37332

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: DNA

A:Residues: 1-33,'E','34'-95,'T','97'-109,'R','111'-205 <EGU>  
C:Genetics:

A:Gene: GDB:BCL2

A:Cross-references: GDB:119031; OMIM:151430  
A:Map position: 18q21.3-18q21.3

C:Function:  
A:Description: blocks apoptosis in hematopoietic cells

C:Superfamily: bcl transforming protein  
C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; pr

Query Match

Best Local Similarity 14.0%; Score 124; DB 1; Length 205;  
Matches 32; Conservative 22; Mismatches 39; Indels 86; Gaps 2;

QY 37 EYVHARLRLAGLSW-----SAPERASPARG----- 61

Db 17 KYIHYKLSQRYEMDAGDADAAPLGAAPPTGIFSFQESNPMRA 76

QY 62 -----GRLAECYV 70

Db 77 APCGAAPALSPVPCVHILTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGFATVVEE 136

QY 71 LRLGITWGVSLYSAAAGLAVDCYRQAPAMVHALVDCLEGFVRK 129

Db 137 LFRDGVNMGRIYAFEEFGVGVCSYVREMSPLVDNIALMTEYLNRHLHTWIDNGW 195

RESULT 7

transferring protein bcl-2-beta - mouse

C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 18-Jun-1999

C:Accession: B25960

R:Negishi, M.; Sillini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.  
Cell 49, 455-463, 1987

A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene ho  
A:Reference number: A90893; MUID:87187643; PMID:3032455

A:Accession: B25960

A:Molecule type: DNA

A:Residues: 1-199 <NEG>

A:Cross-references: GB:M16506; NID:9468335; PIDN:AAA37281.1; PID:9387110

C:Genetics:

A:Gene: BCL2

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; transforming protein

Query Match

Best Local Similarity 13.9%; Score 123; DB 1; Length 199;  
Matches 38; Conservative 24; Mismatches 46; Indels 92; Gaps 4;

QY 28 VAQAKALG-----REYVHARLRLAGLSW-----SAPERASPARG----- 61

Db 1 MAQAGRTGYDNRITWKYIHYKLSQRYEMDAGDADAAPLGAAPPTGIFSFQESNPMRA 60

QY 62 ----- 61

Db 61 VHEMAARTSPRLPLVATAGPALSPVPCVHILTLRRAGDDFSRRYRRDFAEMSSQLHLTP 120

QY 62 ----GRLAECYVTLRLGITWGVSLYSAAAGLAVDCYRQAPAMVHALVDCLEGFVRK 117

Db 121 FTARGFATVVEELFRDGVNMGRIYAFEEFGVGVCSYVREMSPLVDNIALMTEYLNR 180





Db 125 QVYNLEFRDGVNMGRIVAFSEFGALCVESVDKEMOVLVSRIASWMTATYLNDDHLEFWIOE 184  
Qy 126 RSGW 129  
Db 185 NGW 188

Search completed: April 29, 2003, 11:26:37  
Job time : 11.6527 secs

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2003, 11:16:46 ; Search time 25.9661 seconds

(without alignments)  
872.393 Million cell updates/sec

Title: US-09-682-667-8

Perfect score: 884

Sequence: 1 MEVLRRSSVFAEIMDAFDR.....TLCSPGRFLKAFLLPER 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq\_101002.\*  
1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
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4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
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8: /SID2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
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10: /SID2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
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17: /SID2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
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19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	884	100.0	170	20	AAV14156	Human Bcl protein se
2	853	96.5	170	20	AAV14154	Rat Bok protein se
3	852.5	96.4	213	20	AAV14155	Human Bok protein se
4	828.5	93.7	213	20	AAV14153	Rat Bok protein se
5	820.5	92.8	213	21	AAV14144	Human ORFX ORF1208
6	484	54.8	134	22	AAV85665	Human Bcl-2-like p
7	484	54.8	134	21	AAV85665	Human Bcl-2-like p
8	169.5	19.2	247	22	ABB63760	Breast and ovarian
9	169	19.1	846	22	ABB64401	Drosophila melanog
10	135	15.3	272	19	AAV21120	Drosophila melano
						Human bcl2 proto-o

11	134	15.2	239	17	AAW02383	Human BCL2. Homo
12	134	15.2	239	22	AAG64036	Human Bcl-2 protei
13	134	15.2	239	22	AAG64036	Human Bcl-2 protei
14	133	15.0	239	9	AAE80987	Sequence of bcl-2-
15	133	15.0	239	14	AAV42312	Bcl-2 oncogene pro
16	133	15.0	239	16	AAV70331	Human bcl-2 protei
17	133	15.0	239	19	AAV71404	Human bcl-2 alpha
18	133	15.0	239	16	AAV40217	Human bcl-2. Homo
19	133	15.0	239	20	AAV87810	A human Bcl-2 prot
20	133	15.0	239	20	AAV87812	Human Bcl-2 prot
21	133	15.0	239	22	AAE08573	Human Bcl-2 protei
22	133	15.0	239	22	AAG64035	Human Bcl-2 protei
23	133	15.0	239	22	AAG64037	Human Bcl-2 protei
24	133	15.0	239	22	AAV74127	Human bcl-2. Homo
25	133	15.0	239	22	AAV74129	Human bcl-2alpha.
26	133	15.0	239	22	AAV48288	Human BCL-2 protei
27	133	15.0	239	22	AAV35130	Human Bcl-2. Homo
28	133	15.0	239	22	AAV50537	Human Bcl-2 protei
29	133	15.0	239	23	AAV75986	Protein sequence.
30	133	15.0	239	23	AAV76553	Human Bcl-2 poly
31	133	15.0	239	23	AAV05227	Human D34A caspase
32	131	14.8	239	22	AAV64039	Human Bcl-2 protei
33	130	14.7	229	17	AAV01021	Apoptosis-blocking
34	130	14.7	229	20	AAV94348	Human Bcl-2 mutant
35	130	14.7	236	20	AAV87811	A murine Bcl-2 pro
36	130	14.7	236	22	AAV74128	Murine bcl-2. Mus
37	130	14.7	236	22	AAV35131	Murine Bcl-2. Mus
38	130	14.7	236	23	AAV76554	Murine Bcl-2 poly
39	130	14.7	239	15	AAV47344	Human oncogene bcl
40	128.5	14.5	232	17	AAV01020	Apoptosis-blocking
41	128.5	14.5	232	20	AAV94347	Human Bcl-2 mutant
42	125.5	14.2	239	21	AAV69203	Amino acid sequenc
43	125	14.1	239	17	AAV01018	Apoptosis-blocking
44	125	14.1	239	20	AAV94345	Human Bcl-2 wild-t
45	124	14.0	205	16	AAV70332	Human bcl-2 protei

## ALIGNMENTS

RESULT 1  
AAV14156  
ID AAV14156 standard; Protein; 170 AA.  
XX  
AC AAV14156;  
XX  
DT 27-JUL-1999 (first entry)  
XX  
DE Human Bcl protein sequence.  
XX  
XX Bok protein; Bcl-2-related ovarian killer; BHL1 variant; endometriosis;  
KW pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
KW reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
KW ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
XX  
XX Proliferative disorder; human.  
XX  
OS Homo sapiens.  
XX  
XX  
XX PN MO9924453-A1.  
XX  
XX PD 20-MAY-1999.  
XX  
XX PF 04-NOV-1998; 98WO-US23523.  
XX  
XX PR 07-NOV-1997; 97US-0064943.  
XX  
XX (STRD ) UNIV IELAND STANFORD JUNIOR.  
XX  
XX PA Hsu SY, Hsueh AJW.  
XX  
XX PI WPI: 1999-327356/27.  
XX  
XX DR N-PSDB; AAV61106.  
XX

PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
protein and its related gene  
PS Claim 2; Page 57-58; 62pp; English.  
XX  
CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
CC pro-apoptotic Bok-related protein can be introduced into cell populations  
CC to upregulate expression of the proteins in order to induce apoptosis in  
CC the cell population. This is useful for treatment of diseases where there  
CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
CC other tissues, and provide a means for manipulating apoptosis. The Bok  
CC protein and transgenic animal are also useful for identifying ligands or  
CC substrates. Modulation of the gene activity in vivo is useful for  
CC prophylaxis and therapy of, e.g. cancer and other proliferative  
CC disorders. Bok genes are also useful for identification of cell type  
CC based on expression. Identification of Bok as a new pro-apoptotic protein  
CC with wide tissue distribution and heterodimerisation properties  
CC facilitates elucidation of apoptosis mechanisms.  
XX  
SQ Sequence 170 AA:  
Query Match 100.0%; Score 884; DB 20; Length 170;  
Best Local Similarity 100.0%; Pred. No. 4.9e-93;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MEVLRSSVFPAEIMDADRDPTDKELVAQAALGREYVHARLRLAGLSWSAPERASPAP 60  
DB 1 MEVLRSSVFPAEIMDADRDPTDKELVAQAALGREYVHARLRLAGLSWSAPERASPAP 60  
OY 61 GGRLAECVTLRLGITGKVVSLYSAAAGLAVDCVROQAPMVAHALVDCLEEFYRKTIA 120  
DB 61 GGRLAECVTLRLGITGKVVSLYSAAAGLAVDCVROQAPMVAHALVDCLEEFYRKTIA 120  
OY 121 TWLRRGGMTDVLKCVSTKPGFRSHMLVATLCISGFRFLKAFFLLPER 170  
DB 121 TWLRRGGMTDVLKCVSTKPGFRSHMLVATLCISGFRFLKAFFLLPER 170  
RESULT 2  
AAV14154  
ID AAV14154 standard; Protein: 170 AA.  
XX  
AC AAV14154;  
XX  
DT 27-JUL-1999 (first entry)  
XX  
DE Rat Bok protein sequence.  
XX  
KW Bok protein; Bcl-2-related ovarian killer; BH3 variant; endometriosis;  
KW pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
KW reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
KW ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
KW proliferative disorder; rat.  
XX  
OS Rattus rattus.  
XX  
PN WO9924453-A1.  
XX  
PD 20-MAY-1999.  
XX  
PE 04-NOV-1998; 98WO-US23523.  
XX  
PR 07-NOV-1997; 97US-0064943.  
XX  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX  
XX Hsu SY, Hsueh AJW;  
XX

DR WPI; 1999-327356/27.  
DR N-PSDB; AAX61104.  
XX  
PT Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
protein and its related gene  
PS Claim 2; Page 54-55; 62pp; English.  
XX  
CC This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
CC protein, of the invention. Coding sequences for Bok or BH3 variants of  
CC pro-apoptotic Bok-related protein can be introduced into cell populations  
CC to upregulate expression of the proteins in order to induce apoptosis in  
CC the cell population. This is useful for treatment of diseases where there  
CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
CC other tissues, and provide a means for manipulating apoptosis. The Bok  
CC protein and transgenic animal are also useful for identifying ligands or  
CC substrates. Modulation of the gene activity in vivo is useful for  
CC prophylaxis and therapy of, e.g. cancer and other proliferative  
CC disorders. Bok genes are also useful for identification of cell type  
CC based on expression. Identification of Bok as a new pro-apoptotic protein  
CC with wide tissue distribution and heterodimerisation properties  
CC facilitates elucidation of apoptosis mechanisms.  
XX  
SQ Sequence 170 AA:  
Query Match 96.5%; Score 853; DB 20; Length 170;  
Best Local Similarity 97.6%; Pred. No. 1.7e-89;  
Matches 166; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 1 MEVLRSSVFPAEIMDADRDPTDKELVAQAALGREYVHARLRLAGLSWSAPERASPAP 60  
DB 1 MEVLRSSVFPAEIMDADRDPTDKELVAQAALGREYVHARLRLAGLSWSAPERASPAP 60  
OY 61 GGRLAECVTLRLGITGKVVSLYSAAAGLAVDCVROQAPMVAHALVDCLEEFYRKTIA 120  
DB 61 GGRLAECVTLRLGITGKVVSLYSAAAGLAVDCVROQAPMVAHALVDCLEEFYRKTIA 120  
OY 121 TWLRRGGMTDVLKCVSTKPGFRSHMLVATLCISGFRFLKAFFLLPER 170  
DB 121 TWLRRGGMTDVLKCVSTKPGFRSHMLVATLCISGFRFLKAFFLLPER 170  
RESULT 3  
AAV14155  
ID AAV14155 standard; Protein: 213 AA.  
XX  
AC AAV14155;  
XX  
DT 27-JUL-1999 (first entry)  
XX  
DE Human Bok protein sequence.  
XX  
KW Human Bok protein.  
KW Bok protein; Bcl-2-related ovarian killer; BH3 variant; endometriosis;  
KW pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
KW reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
KW ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
KW proliferative disorder; human.  
XX  
OS Homo sapiens.  
XX  
PN WO9924453-A1.  
XX  
PD 20-MAY-1999.  
XX  
PE 04-NOV-1998; 98WO-US23523.  
XX  
PR 07-NOV-1997; 97US-0064943.  
XX  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX

XX Hsu SY, Hsueh AJW;  
 PI  
 XX WPI: 1999-327356/27.  
 DR N-PSDB: AAX61105.  
 DR  
 XX Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
 PT protein and its related gene  
 PT  
 XX Claim 2; Page 55-56; 62pp; English.  
 PS  
 XX This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
 CC protein, of the invention. Coding sequences for Bok or BH31 variants of  
 CC pro-apoptotic Bok-related protein can be introduced into cell populations  
 CC to upregulate expression of the proteins in order to induce apoptosis in  
 CC the cell population. This is useful for treatment of diseases where there  
 CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
 CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
 CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
 CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
 CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
 CC other tissues, and provide a means for manipulating apoptosis. The Bok  
 CC protein and transgenic animal are also useful for identifying ligands or  
 CC substrates. Modulation of the gene activity in vivo is useful for  
 CC prophylaxis and therapy of, e.g. cancer and other proliferative  
 CC disorders. Bok genes are also useful for identification of cell type  
 CC based on expression. Identification of Bok as a new pro-apoptotic protein  
 CC with wide tissue distribution and heterodimerisation properties  
 CC facilitates elucidation of apoptosis mechanisms.  
 CC  
 XX Sequence 213 AA;  
 SQ  
 Query Match 96.4%; Score 852.5; DB 20; Length 213;  
 Best Local Similarity 79.8%; Pred. No. 2.6e-89;  
 Matches 170; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

QY 1 MEVLRSSVFAEIMDAFDRMPTDKELVAQAKALGREYVHARLRLAGLSMSAPERASAP 60  
 DB 1 MEVLRSSVFAEIMDAFDRMPTDKELVAQAKALGREYVHARLRLAGLSMSAPERASAP 60  
 QY 61 GGRLAEVCTVLLRL-----GTT 77  
 DB 61 GGRLAEVCTVLLRLDELEQIRPSYRVNVARQLHPLQSEPVVTD AFLAVAGHIFSAGIT 120  
 QY 78 WGVVSVLSAAGLAVDCVROQOPAMVHALVDCLEFVRKTLATWLRRGGWTDLKCV 137  
 DB 121 WGVVSVLSAAGLAVDCVROQOPAMVHALVDCLEFVRKTLATWLRRGGWTDLKCV 180  
 QY 138 STKPGFRSHMLVATLCSFGRLKAFLLPPER 170  
 DB 181 STKPGFRSHMLVATLCSFGRLKAFLLPPER 213

RESULT 4  
 AAY14153  
 ID AAY14153 standard; Protein: 213 AA.  
 AC AAY14153;  
 XX  
 XX 27-JUL-1999 (first entry)  
 DT  
 XX  
 DE Rat Bok protein sequence.  
 XX  
 KW Bok protein; Bcl-2-related ovarian killer; BH31 variant; endometriosis;  
 KW pro-apoptotic protein; apoptosis inducer; hyperproliferation disease;  
 KW reproductive tissue; uterine carcinoma; testicular carcinoma; cervix;  
 KW ovarian carcinoma; glandular epithelial carcinoma; cancer; therapy;  
 KW proliferative disorder; rat.  
 XX  
 OS Rattus rattus.  
 XX  
 XX W09924453-A1.  
 FM  
 XX

PD 20-MAY-1999;  
 XX  
 XX 04-NOV-1998; 98WO-US23523.  
 XX  
 XX 07-NOV-1997; 97US-0064943.  
 XX  
 XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PA  
 XX Hsu SY, Hsueh AJW;  
 PI  
 XX WPI: 1999-327356/27.  
 DR N-PSDB: AAX61103.  
 DR  
 XX Mammalian Bok (Bcl-2-related ovarian killer), a pro-apoptotic  
 PT protein and its related gene  
 PT  
 XX Claim 2; Page 53-54; 62pp; English.  
 PS  
 XX This sequence is a mammalian Bok (Bcl-2-related ovarian killer)  
 CC protein, of the invention. Coding sequences for Bok or BH31 variants of  
 CC pro-apoptotic Bok-related protein can be introduced into cell populations  
 CC to upregulate expression of the proteins in order to induce apoptosis in  
 CC the cell population. This is useful for treatment of diseases where there  
 CC is hyperproliferation of reproductive tissue, e.g. uterine, testicular  
 CC and ovarian carcinomas, endometriosis, squamous and glandular epithelial  
 CC carcinomas of the cervix. Cell killing induced by Bok can be suppressed  
 CC by co-expression with selective anti-apoptotic Bcl-2 proteins. The Bok  
 CC protein can be used to elucidate apoptosis mechanisms in reproductive and  
 CC other tissues, and provide a means for manipulating apoptosis. The Bok  
 CC protein and transgenic animal are also useful for identifying ligands or  
 CC substrates. Modulation of the gene activity in vivo is useful for  
 CC prophylaxis and therapy of, e.g. cancer and other proliferative  
 CC disorders. Bok genes are also useful for identification of cell type  
 CC based on expression. Identification of Bok as a new pro-apoptotic protein  
 CC with wide tissue distribution and heterodimerisation properties  
 CC facilitates elucidation of apoptosis mechanisms.  
 CC  
 XX Sequence 213 AA;  
 SQ  
 Query Match 93.7%; Score 828.5; DB 20; Length 213;  
 Best Local Similarity 78.4%; Pred. No. 1.5e-86;  
 Matches 167; Conservative 0; Mismatches 3; Indels 43; Gaps 1;

QY 1 MEVLRSSVFAEIMDAFDRMPTDKELVAQAKALGREYVHARLRLAGLSMSAPERASAP 60  
 DB 1 MEVLRSSVFAEIMDAFDRMPTDKELVAQAKALGREYVHARLRLAGLSMSAPERASAP 60  
 QY 61 GGRLAEVCTVLLRL-----GTT 77  
 DB 61 GGRLAEVCTVLLRLDELEQIRPSYRVNVARQLHPLQSEPVVTD AFLAVAGHIFSAGIT 120  
 QY 78 WGVVSVLSAAGLAVDCVROQOPAMVHALVDCLEFVRKTLATWLRRGGWTDLKCV 137  
 DB 121 WGVVSVLSAAGLAVDCVROQOPAMVHALVDCLEFVRKTLATWLRRGGWTDLKCV 180  
 QY 138 STKPGFRSHMLVATLCSFGRLKAFLLPPER 170  
 DB 181 STKPGFRSHMLVATLCSFGRLKAFLLPPER 213

RESULT 5  
 AAB41444  
 ID AAB41444 standard; Protein: 213 AA.  
 AC AAB41444;  
 XX  
 XX 08-FEB-2001 (first entry)  
 DT  
 XX  
 DE Human ORFX ORF1208 polypeptide sequence SEQ ID NO:2416.  
 XX  
 KW Human; open reading frame; ORFX; detection; cytosolic; hepatotropic;  
 KW vulnary; antiproliferative; antiparkinsonian; neuroprotective;  
 KW anticonvulsant; osteoplastic; antiarthritic; immunosuppressant; cardiac;





```

Db      11 AROLHISL-----QSEPVVTDALFVAGHIFSAGITGKVSLSYVAAGLAVDCVROAQ 64
Qy      101 PAMVHALVDCGFEVFRKTLATWLRRRGGMTDVLKCVSTKGFPSHMLVATLCSFGRELK 160
Db      65 PAMVHALVDCGFEVFRKTLATWLRRRGGMTDVLKCVSTDGLRSHMLVVALCSFGRELK 124
Qy      161 AAFVLLPER 170
Db      125 AAFVLLPER 134

RESULT 7
AAB58949
ID AAB58949 standard; Protein; 176 AA.
AC AAB58949;
DT 27-MAR-2001 (first entry)
XX
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 657.
XX
KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW neurotropic; neuriprotective; antiviral; antiatherogenic; hepatotropic;
KW antidiabetic; antihistaminic; antitumor; antileukemic; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease.
XX
OS Homo sapiens.
XX
PN WO20005173-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05881.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI: 2000-611515/58.
XX
DR N-PSDB: AAF21852.
XX
XX
FT New human breast and ovarian cancer associated gene sequences and the
FT polypeptides encoded by these genes, useful in the prevention,
FT treatment and diagnosis of cancer, immune disorders, cardiovascular
FT disorders and neurological diseases -
PT
PT
XX
PS Claim 11; Page 1103; 1299pp; English.
XX
XX
CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC associated with breast and ovarian cancer. Included in the invention are
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC isolation and characterisation of the DNA and protein sequences of the
CC invention. The breast and ovarian cancer associated DNA, protein, agonist
CC or antagonist sequences exhibit cytostatic; immunosuppressive;
CC neurotropic; neuriprotective; antiviral; antiallergic; hepatotropic;
CC antidiabetic; antihistaminic; antitumor; antileukemic; anticonvulsant;
CC antibacterial; antifungal; antiparasitic and cardiac activity. The
CC polynucleotide and protein sequences are used in the diagnosis of cancer,
CC particularly breast and ovarian cancer. The nucleic acid sequences,
CC proteins, agonists and antagonists may also be used in the diagnosis,
CC prevention and treatment of immune disorders e.g. Addison's disease,
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; cardiovascular disorders such as
CC myocardial ischaemias; wound healing; neurological diseases such as

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CC cerebral anoxia and epilepsy; and infectious diseases.
XX
SQ Sequence 176 AA;
Query Match 54.8%; Score 484; DB 21; Length 176;
Best Local Similarity 73.8%; Pred. No. 3.2e-47;
Matches 96; Conservative 5; Mismatches 23; Indels 1; Gaps 1;

Qy      41 ARLRAGISWSAPERASAPGRLAEVCTVLRIGITGKVSLSYVAAGLAVDCVROAQ 100
Db      53 AROLHISL-----QSEPVVTDALFVAGHIFSAGITGKVSLSYVAAGLAVDCVROAQ 106
Qy      101 PAMVHALVDCGFEVFRKTLATWLRRRGGMTDVLKCVSTKGFPSHMLVATLCSFGRELK 160
Db      107 PAMVHALVDCGFEVFRKTLATWLRRRGGMTDVLKCVSTDGLRSHMLVVALCSFGRELK 166
Qy      161 AAFVLLPER 170
Db      167 AAFVLLPER 176

RESULT 8
AAB63760
ID AAB63760 standard; Protein; 247 AA.
AC AAB63760;
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 18072.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI: 2001-656860/75.
XX
DR N-PSDB: ABL07863.
XX
XX
FT New isolated nucleic acid detection reagent for detecting 1000 or more
FT genes from Drosophila and for elucidating cell signalling and cell-cell
FT interactions -
PT
PT
XX
PS Disclosure; SEQ ID NO 18072; 21pp + Sequence Listing; English.
XX
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB101840-AB116175) and the encoded proteins
CC (AAB57737-AB12072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 247 AA;
Query Match 19.2%; Score 169.5; DB 22; Length 247;

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Best Local Similarity 27.8%; Pred. No. 5.2e-11;  
Matches 44; Conservative 19; Mismatches 42; Indels 53; Gaps 4;

QY 25 KEIYAQAKALGREYHARLRAGL-----SWSAP----- 53  
Db 87 QDIISGRCICGHIKRRRLRSGLFNKKLGIRISLGSKGIADVPAVOVLDEL 146  
QY 54 ERASPA-----PGGR-----LAECTVLRLGITWGVVSLYSAAGL 91  
Db 147 ERMHPIRYNGVAROICRNPGSEFHTPDVAVSLILGAVGRELFREVEITWSKVISLFAIAGL 206

QY 92 AYDCVROAPAMVHALVDCLGFEFVKTLATWLRRCGM 129  
Db 207 SVDCVROGHPEYLPKLMESVSEVIEDELVPWINENGW 244

RESULT 9  
ABB64401  
ID ABB64401 standard; Protein; 846 AA.  
XX  
AC ABB64401;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster polypeptide SEQ ID NO 19995.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical.  
XX  
OS Drosophila melanogaster.  
XX  
PN MO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001MO-US09231.  
XX  
PR 23-MAR-2000; 2000US-191637P.  
PR 11-JUL-2000; 2000US-0614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
DR WPI: 2001-656860/75.  
DR N-PSDB; ABL08504.  
XX  
PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -  
XX  
PS Disclosure; SEQ ID NO 19995; 21pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (AB101840-AB116175), expressed DNA  
CC sequences (AB101840-AB116175) and the encoded proteins  
CC (AB857737-AB872072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 846 AA;

Query Match 19.1%; Score 169; DB 22; Length 846;  
Best Local Similarity 27.6%; Pred. No. 2.9e-10;  
Matches 43; Conservative 17; Mismatches 44; Indels 52; Gaps 3;

26 ELVAQAKALGREYHARLRAG-LSMSAPER----- 55  
::: | | | : | | | | | | : |

Db 96 DIINQKCLGQYIRANLRRAVLNRKVOTLRNIIDPGSSHVYEVFPALNSKEELER 155  
QY 56 -----ASPAGGRLAE-----VCTVLRIGITWGVVSLYSAAGLAV 93  
Db 156 MHPRVYTNISQSLRAPFGELEDSDMAPMLNLVAKLFPSSITWGNIIISFVCGGFAI 215  
QY 94 DCVROAPAMVHALVDCLGFEFVKTLATWLRRCGM 129  
Db 216 DCVROGHFDYLOCLIDGLAEIIEEDLVYWLIDNGW 251

RESULT 10  
AAV21120  
ID AAV21120 standard; Protein; 272 AA.  
XX  
AC AAV21120;  
XX  
DT 22-JUL-1999 (first entry)  
XX  
DE Human bcl2 proto-oncogene wild type protein fragment 17.  
XX  
KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
KW frameshift mutation; age-related disease; neurodegenerative disorder;  
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;  
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
KW high mobility group protein-C; neuroendocrine specific protein A.  
XX  
OS Homo sapiens.  
XX  
PN MO9845322-A2.  
XX  
PD 15-OCT-1998.  
XX  
PE 02-APR-1998; 98MO-IB00705.  
XX  
PR 10-APR-1997; 97US-0043163.  
XX  
PA (UYUT-) RIJKSUNIV UTRECHT.  
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.  
PA (UYRO-) UNIV ROTTERDAM ERASMUS.  
XX  
PI Burbach JPH, Grosveld FG, Van Leeuwen FW;  
XX  
DR WPI: 1998-609901/51.  
DR N-PSDB; AAX75766.  
XX  
PT Diagnosing disease by detecting frameshift mutations in RNA or  
PT corresponding protein mutations - used to diagnose cancer and  
PT neurological diseases, particularly Alzheimer's disease, and also  
PT for treatment and prevention with specific ribozymes or wild-type  
PT RNA  
XX  
PS Disclosure; Figure 15; 258pp; English.  
XX  
CC This invention describes a novel method for the diagnosis of a disease  
CC caused by, or associated with, an RNA molecule that has a frameshift  
CC mutation. The method is used to diagnose age-related diseases, especially  
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,  
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
CC and many others listed) or susceptibility to these disorders. The method  
CC allows a definitive diagnosis of Alzheimer's disease in living patients,  
CC at an early stage. It is based on the observation that disease may be  
CC caused by mutations in RNA rather than DNA. The invention describes the  
CC use of neuronal system RNA molecules, specifically proteins including  
CC beta-amyloid precursor protein (beta-APP), the microtubule associated  
CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule  
CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,



CC Bcl-2 protein of the invention.  
 XX  
 SQ Sequence 239 AA;  
 Query Match 15.2%; Score 134; DB 22; Length 239;  
 Best Local Similarity 19.4%; Pred. No. 5.8e-07;  
 Matches 40; Conservative 26; Mismatches 52; Indels 88; Gaps 4;  
 QY 37 EYVHARLLRAGLSW-----SAPERASAPG----- 61  
 Db 17 KYIHVKLAGGYEMDADGVGAAPGAPAPGIFSSQPGHPPHAPASDPVARTSPLOTPTA 76  
 QY 62 -----GRLAEVCTV 70  
 Db 77 APGAAGPALSPVPVYVHLLRQAGDDFSRRYRGDFEAMSSQLHLTPPTARGREATVVEE 136  
 QY 71 LLRLGITWGVKVSLSYSAAGIAYDCVROAOPAMVHALVDCIGFEFVKTLATWLRRCGWT 130  
 Db 137 LFRDGVWVGRIYVAFEEFGVWCVEAVNREMSPLVDNALMWTETLNHNLHTWIDNGGWD 196  
 QY 131 DVLCV-VSTKPGFRSHWL-VATLCS 154  
 Db 197 AFVELYGPMSRPLDFEWSLSKTLIS 222  
 RESULT 13  
 AAG64038  
 ID AAG64038 standard; protein; 239 AA.  
 XX  
 AC AAG64038;  
 XX  
 DT 10-SEP-2001 (first entry)  
 XX  
 DE Human Bcl-2 protein mutant #3.  
 XX  
 KW Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200142459-A1.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 07-DEC-2000; 2000WO-JP08667.  
 XX  
 PR 09-DEC-1999; 99JP-0350427.  
 XX  
 PA (HISM ) HISAMITSU PHARM CO LTD.  
 XX  
 PI Shibazaki F, Kuma H;  
 XX  
 DR WPI; 2001-381681/40.  
 XX  
 PT New apoptosis inhibitors, useful for treating apoptosis related  
 PT disorders -  
 PS Claim 7; Page 33-34; 43pp; Japanese.  
 XX  
 CC The invention relates to an apoptosis inhibitor comprising the  
 CC amino acid sequence of Bcl-2 protein in which at least one serine  
 CC residue is substituted by alanine or aspartic acid. The protein has  
 CC increased apoptosis inhibitory activity compared with the wild type  
 CC Bcl-2 protein. The mutated Bcl-2 protein is useful in the treatment  
 CC of disorders caused by apoptosis. The present sequence is a mutant  
 CC Bcl-2 protein of the invention.  
 CC  
 SQ Sequence 239 AA;  
 Query Match 15.2%; Score 134; DB 22; Length 239;  
 Best Local Similarity 19.4%; Pred. No. 5.8e-07;  
 Matches 40; Conservative 26; Mismatches 52; Indels 88; Gaps 4;

QY 37 EYVHARLLRAGLSW-----SAPERASAPG----- 61  
 Db 17 KYIHVKLAGGYEMDADGVGAAPGAPAPGIFSSQPGHPPHAPASDPVARTSPLOTPTA 76  
 QY 62 -----GRLAEVCTV 70  
 Db 77 APGAAGPALSPVPVYVHLLRQAGDDFSRRYRGDFEAMSSQLHLTPPTARGREATVVEE 136  
 QY 71 LLRLGITWGVKVSLSYSAAGIAYDCVROAOPAMVHALVDCIGFEFVKTLATWLRRCGWT 130  
 Db 137 LFRDGVWVGRIYVAFEEFGVWCVEAVNREMSPLVDNALMWTETLNHNLHTWIDNGGWD 196  
 QY 131 DVLCV-VSTKPGFRSHWL-VATLCS 154  
 Db 197 AFVELYGPMSRPLDFEWSLSKTLIS 222  
 RESULT 14  
 AAP80987  
 ID AAP80987 standard; protein; 239 AA.  
 XX  
 AC AAP80987;  
 XX  
 DT 17-DEC-1990 (first entry)  
 XX  
 DE Sequence of bcl-2-alpha encoded by sequence of bcl-2 cDNA corresp. to  
 DE the 5.5 kb transcript.  
 XX  
 KW B-cell neoplasm; diagnosis; follicular lymphomas.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP252685-A.  
 XX  
 PD 13-JAN-1988.  
 XX  
 PF 02-JUL-1987; 87EP-0305863.  
 XX  
 PR 09-JUL-1986; 86US-0883687.  
 XX  
 PA (WIST-) WISTAR CORP.  
 XX  
 PI Tsujimoto Y, Croce CM;  
 XX  
 DR WPI; 1988-008633/02.  
 XX  
 DR N-PADB; AAN81292.  
 XX  
 PT Detection of B-cell neoplasms -  
 PT by extn. of proteins or RNA from B-cells and quantitation using  
 PT specific antibody or DNA probe  
 PS Claim 12; Fig 2A-2D; 23pp; English.  
 XX  
 CC A human bcl-2 gene substantially free of introns is claimed. Also  
 CC claimed is a substantially pure preparation of a protein having an  
 CC N-terminal end encoded by the first exon of the human bcl-2 gene wherein  
 CC said protein is bcl-2-alpha having about 239 (AAP80987) or 205 (AAP80988)  
 CC amino acid residues. B-cell neoplasms which are associated with t(14;18)  
 CC chromosome translocations cause an increase in expression of both the  
 CC mRNA and the protein prods. of the bcl-2 gene. This is used to detect  
 CC B-cell neoplasms including follicular lymphomas as well as other  
 CC lymphomas. Bacterial isolates available as ATCC 67147 and 67148 can be  
 CC used to express bcl-2 gene products alpha (AAN81292) and beta (AAN91293)  
 CC resp. in bacteria.  
 CC  
 SQ Sequence 239 AA;  
 Query Match 15.0%; Score 133; DB 9; Length 239;  
 Best Local Similarity 19.4%; Pred. No. 7.5e-07;  
 Matches 40; Conservative 26; Mismatches 52; Indels 88; Gaps 4;  
 QY 37 EYVHARLLRAGLSW-----SAPERASAPG----- 61



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